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| FORM PTO-1390 (REV 11-98) | | U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE | | ATTORNEY'S DOCKET NUMBER 127-01 | |
| TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371 | | | | U.S. APPLICATION NO. (if known, see 37 CFR 1.5) 10/018418 | |
| INTERNATIONAL APPLICATION NO. PCT/AU00/00385 | | INTERNATIONAL FILING DATE 28 April 2000 (28.04.00) | | PRIORITY DATE CLAIMED 29 April 1999 (29.04.99) | |
| TITLE OF INVENTION NOVEL GENES ENCODING WHEAT STARCH SYNTHASES AND USES THEREFOR GENES ENCODING WHEAT STARCH SYNTHASES AND USES THEREFOR (as amended) | | | | | |
| APPLICANT(S) FOR DO/EO/US Matthew MORELL, Zhongyi LI, Sadequr RAHMAN, Rudolph APPELS | | | | | |
| Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information: | | | | | |
| 1. <input checked="" type="checkbox"/> This is a FIRST submission of items concerning a filing under 35 U.S.C. 371. 2. <input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371. 3. <input type="checkbox"/> This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1). 4. <input checked="" type="checkbox"/> A proper Demand for International Preliminary Examination was made by the 19 th month from the earliest claimed priority date. 5. <input checked="" type="checkbox"/> A copy of the International application as filed (35 U.S.C. 371(c)(2)) a. <input type="checkbox"/> is transmitted herewith (required only if not transmitted by the International Bureau). b. <input checked="" type="checkbox"/> has been transmitted by the International Bureau. c. <input type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US). 6. <input type="checkbox"/> A translation of the International Application into English (35 U.S.C. 371(c)(2)). 7. <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)): a. <input type="checkbox"/> are transmitted herewith (required only if not transmitted by the International Bureau). b. <input type="checkbox"/> have been transmitted by the International Bureau. c. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired. d. <input checked="" type="checkbox"/> have not been made and will not be made. 8. <input type="checkbox"/> A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)). 9. <input type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)). 10. <input type="checkbox"/> A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)). | | | | | |
| Items 11. To 16. below concern document(s) or information included: | | | | | |
| 11. <input type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98. 12. <input type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included. 13. <input checked="" type="checkbox"/> A FIRST preliminary amendment. <input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment 14. <input type="checkbox"/> A substitute specification. 15. <input type="checkbox"/> A change of power of attorney and/or address letter. 16. <input checked="" type="checkbox"/> Other items or information: Sequence Listing on diskette (write protected) Sequence Listing as paper copy (pages 1--67) Statement under 37 CFR 1.821-1825 | | | | | |
| I hereby certify that this correspondence is being deposited with the United States Postal Service as "Express Mail" in an envelope addressed to: Commissioner of Patents and Trademarks, Washington, D.C. 20231 on <u>29 October 2001</u> (Date of Deposit) <u>B. Kroge</u> Name of Applicant, Assignee or Registered Representative <u>B. Kroge</u> Signature <u>29 October 2001</u> Date of signature <u>EL 527 990 190 US</u> Express Mail Receipt No. | | | | | |

(January 1999)

| | | | | | |
|---|--------------|---|-----------|---|----|
| U.S. APPLICATION NO. (if known, see 37 CFR 1.5) <div style="font-size: 1.5em; font-weight: bold;">10/018418</div> | | INTERNATIONAL APPLICATION NO. PCT/AU00/00385 | | ATTORNEY'S DOCKET NUMBER 127-01 | |
| 17. <input checked="" type="checkbox"/> The following fees are submitted: BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5)): Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO \$1040.00 International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO \$890.00 International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$740.00 International preliminary examination fee paid to USPTO (37 CFR 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4) \$710.00 International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4) \$100.00 <div style="text-align: right;">ENTER APPROPRIATE BASIC FEE AMOUNT =</div> | | | | CALCULATIONS PTO USE ONLY | |
| Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e)). | | | | \$ 1,040 | |
| CLAIMS | NUMBER FILED | NUMBER EXTRA | RATE | \$ | |
| Total claims | 66-20 = | 46 | X \$18.00 | \$ 828 | |
| Independent claims | 5-3 = | 2 | X \$78.00 | \$ 156 | |
| MULTIPLE DEPENDENT CLAIM(S) (if applicable) | | | +\$260.00 | \$ | |
| TOTAL OF ABOVE CALCULATIONS = | | | | \$ 2,154 | |
| Reduction of 1/2 for filing by small entity, if applicable. A Small Entity Statement must also be filed (Note 37 CFR 1.9, 1.27, 1.28). | | | | \$ N/A | |
| SUBTOTAL = | | | | \$ | |
| Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)). | | | | \$ N/A | |
| TOTAL NATIONAL FEE = | | | | \$ | |
| Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property | | | | \$ N/A | |
| TOTAL FEES ENCLOSED = | | | | \$ 2,154 | |
| | | | | Amount to be: | \$ |
| | | | | refunded | |
| | | | | charged | \$ |
| | | | | | |
| a. <input checked="" type="checkbox"/> A check in the amount of \$2,154.00 to cover the above fees is enclosed. b. <input type="checkbox"/> Please charge my Deposit Account No. 07-1969 in the amount of \$_____ to cover the above fees. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 07-1969 . A duplicate copy of this sheet is enclosed. | | | | | |
| NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status. | | | | | |
| SEND ALL CORRESPONDENCE TO: GREENLEE, WINNER and SULLIVAN, P.C. 5370 Manhattan Circle, Suite 201 Boulder, CO 80303 Phone: 303-499-8080 Fax: 303-499-8089 | | | | | |
| | | | | <div style="text-align: center;"> SIGNATURE </div> <div style="display: flex; justify-content: space-between; margin-top: 10px;"> Name: Donna M. Ferber Registration No.: 33,878 </div> | |

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: :
Morrell et al. : Group Art Unit: Not yet assigned
Serial No: Not yet assigned : Examiner: Not yet assigned
Filed: October 29, 2001
For: GENES ENCODING WHEAT STARCH
SYNTHASES AND USES THEREFOR
(as amended)

| CERTIFICATE OF MAILING | |
|--|----------|
| I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as EXPRESS MAIL in an envelope addressed to the Commissioner for Patents, Washington, D.C. 20231. | |
| 29 October 2001 | B. Kroge |
| Date | B. Kroge |
| Express Mail Receipt No: EL 827 990 190 US | |

PRELIMINARY AMENDMENT

Commissioner for Patents
Washington, D.C. 20231

Sir:

Please enter the following amendments:

In the Title:

Rewrite the title as follows:

Genes Encoding Wheat Starch Synthases and Uses Therefor

In the Claims:

Rewrite claims 22, 26, 28, 32, 33, 41, 43, 44, 46, 47, 50, 52, 53, 54, 57 and 59 as follows:

22. (Once amended) A method comprising:

- (i) hybridising single-stranded or double-stranded mRNA, cDNA or genomic DNA with a nucleotide sequence selected from the group consisting of:
 - (a) the nucleotide sequence according to any one of claim 1;

- (b) a probe or primer derived from a nucleotide sequence according to subparagraph (a) and comprising at least about 15 contiguous nucleotides of said nucleotide sequence in length; and
 - (ii) detecting the hybridised mRNA, cDNA or genomic DNA using a detecting means.
- 26. (Once amended) A method of assaying for the presence or absence of a wheat starch synthase polypeptide in a plant or a plant extract or isolated nucleic acid sample, said method at least comprising performing the method according to claim 22.
- 28. (Once amended) A method of marker-assisted breeding and/or selection of a plant at least comprising performing the method according to claim 22.
- 32. (Once amended) A plant produced by the method according to claim 28 wherein said plant expresses a wheat starch synthase polypeptide at a desired level detectable using said method.
- 33. (Once amended) A method of modifying the starch content and/or starch composition of one or more tissues or organs of a plant, comprising expressing in said plant a nucleic acid molecule for a time and under conditions sufficient for the enzyme activity of one or more starch synthase isoenzymes to be modified, wherein said nucleic acid molecule is selected from the group consisting of:
 - (i) the isolated nucleic acid molecule according to claim 1;
 - (ii) a fragment of (i) which comprises a nucleotide sequence capable of being expressed to down-regulate the expression of an endogenous wheat starch synthase isoenzyme of said plant; and
 - (iii) a fragment of (i) which encodes a functional wheat starch synthase isoenzyme of said plant.
- 41. (Once amended) A plant carrying the isolated nucleic acid molecule according to claim 1 as an exogenous complement to its genome
- 43. (Once amended) A propagule of the plant according to claim 41 wherein said propagule carries the introduced nucleic acid molecule present in said plant.

44. (Once amended) A gene construct or vector which comprises the isolated nucleic acid molecule according to claim 1 and one or more origins of replication
46. (Once amended) A gene construct or vector which comprises the probe or primer according to claim 10 and one or more origins of replication.
47. (Once amended) A modified starch derived from the plant according to claim 32 wherein said starch is modified by virtue of the use of the isolated nucleic acid according to claim 1 to produce said plant.
50. (Once amended) A food product comprising the modified starch according to claim 47.
52. (Once amended) The food product according to claim 50 selected from the group consisting of: flour-based sauce; leavened bread; unleavened bread; pasta, noodle; cereal; snack food; cake; and pastry.
53. (Once amended) Use of the modified starch according to claim 47 in the preparation of a food product for consumption by an animal or human.
54. (Once amended) A modified protein derived from the plant according to claim 32 wherein said protein is modified by virtue of the use of the isolated nucleic acid according to claim 1 to produce said plant.
57. (Once amended) A non-food product comprising the modified protein according to claim 54.
59. (Once amended) Use of the modified protein according to claim 54 in the preparation of a non-food product.

Please add the following new claims 60 - 66:

60. (New) A modified starch derived from the plant according to claim 41 wherein said starch is modified by virtue of the use of the isolated nucleic acid according to claim 1 to produce said plant.
61. (New) A food product comprising the modified starch according to claim 60.

62. (New) The food product according to claim 61 consisting of flour or a flour-based food product
63. (New) A modified protein derived from the plant according to claim 41 wherein said protein is modified by virtue of the use of the isolated nucleic acid according to claim 1 to produce said plant.
64. (New) A non-food product comprising the modified protein according to claim 63.
65. (New) The non-food product according to claim 57 selected from the group consisting of: films; coatings; adhesives; building materials; and packaging materials
66. (New) Use of the modified protein according to claim 63 in the preparation of a non-food product.

In the Sequence Listing:

Delete pages 1-59 of the existing Sequence Listing as filed in PCT/AU00/00385 and replace with new Sequence Listing pages 1-67.

REMARKS

The title has been amended to delete the initial word "Novel."

Claims 22, 26, 28, 32, 33, 41, 43, 44, 46, 47, 50, 52, 53, 54, 57 and 59 have amended to remove multiple dependency. New claims 60-66, which are supported by the original claims prior to the present amendment, have been entered. None of the amendments made herein constitutes the addition of new matter.

The Sequence Listing has been rewritten to U.S. Patent Office rules. All sequence information was present in the Sequence Listing which was part of PCT AU00/00385. Accordingly the present submission does not add new matter.

Conclusion

In view of the foregoing, it is submitted that this case is in condition for allowance, and passage to issuance is respectfully requested.

If there are any outstanding issues related to patentability, the courtesy of a telephone interview is requested, and the Examiner is invited to call to arrange a mutually convenient time.

It is believed that this amendment does not necessitate the payment of any fees under 37 C.F.R. 1.16-1.17. If this is incorrect, however, please charge any fee due under the foregoing Rules to Deposit Account No. 07-1969.

Respectfully submitted,



Donna M. Ferber
Reg. No. 33,878

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Attorney docket No.127-01
bmk: October 29, 2001

Marked up version of amended paragraph(s) and claim(s) in attached Amendment.

Docket No.: 127-01
 Filed: October 29, 2001

In the Title:

[Novel] Genes Encoding Wheat Starch Synthases and Uses Therefor

In the claims:

22. (Once amended) A method comprising:
 - (i) hybridising single-stranded or double-stranded mRNA, cDNA or genomic DNA with a nucleotide sequence selected from the group consisting of:
 - (a) the nucleotide sequence according to [any one of claims 1 to 9] claim 1;
 - (b) a probe or primer derived from a nucleotide sequence according to subparagraph (a) and comprising at least about 15 contiguous nucleotides of said nucleotide sequence in length; and
 - (ii) detecting the hybridised mRNA, cDNA or genomic DNA using a detecting means.
26. (Once amended) A method of assaying for the presence or absence of a wheat starch synthase polypeptide in a plant or a plant extract or isolated nucleic acid sample, said method at least comprising performing the method according to [any one of claims 22 to 25.] claim 22.
28. (Once amended) A method of marker-assisted breeding and/or selection of a plant at least comprising performing the method according to [any one of claims 22 to 25.] claim 22.
32. (Once amended) A plant produced by the method according to [any one of claims 28 to 31] claim 28 wherein said plant expresses a wheat starch synthase polypeptide at a desired level detectable using said method.
33. (Once amended) A method of modifying the starch content and/or starch composition of one or more tissues or organs of a plant, comprising expressing in said plant a nucleic acid molecule for a time and under conditions sufficient for the enzyme activity of one or more starch synthase isoenzymes to be modified, wherein said nucleic acid molecule is selected from the group consisting of:
 - (i) the isolated nucleic acid molecule according to [any one of claims 1 to 9;] claim 1;
 - (ii) a fragment of (i) which comprises a nucleotide sequence capable of being expressed to down-regulate the expression of an endogenous wheat starch synthase isoenzyme of said plant; and
 - (iii) a fragment of (i) which encodes a functional wheat starch synthase isoenzyme of said plant.
41. (Once amended) A plant carrying the isolated nucleic acid molecule according to [ny one of claims 1 to 9] claim 1 as an exogenous complement to its genome

43. (Once amended) A propagule of the plant according to claim 41 [or 42] wherein said propagule carries the introduced nucleic acid molecule present in said plant.
44. (Once amended) A gene construct or vector which comprises the isolated nucleic acid molecule according to [any one of claims 1 to 9] claim 1 and one or more origins of replication
46. (Once amended) A gene construct or vector which comprises the probe or primer according to claim 10 [or 11] and one or more origins of replication.
47. (Once amended) A modified starch derived from the plant according to claim 32 [or 41] wherein said starch is modified by virtue of the use of the isolated nucleic acid according to claim 1 to produce said plant.
50. (Once amended) A food product comprising the modified starch according to [any one of claims 47 to 49.] claim 47.
52. (Once amended) The food product according to claim 50 [or 51] selected from the group consisting of: flour-based sauce; leavened bread; unleavened bread; pasta, noodle; cereal; snack food; cake; and pastry.
53. (Once amended) Use of the modified starch according to [any one of claims 47 to 49] claim 47 in the preparation of a food product for consumption by an animal or human.
54. (Once amended) A modified protein derived from the plant according to claim 32 [or 41] wherein said protein is modified by virtue of the use of the isolated nucleic acid according to claim 1 to produce said plant.
57. (Once amended) A non-food product comprising the modified protein according to [any one of claims 54 to 56.] claim 54.
59. (Once amended) Use of the modified protein according to [any one of claims 54 to 56] claim 54 in the preparation of a non-food product.

SEQUENCE LISTING

<110> Morell, Matthew
Li, Zhongyi
Rahman, Sadequr
Appels, Rudolph

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Gly Trp Thr Phe Asp Arg Ala Glu Ala Gln Lys Leu Ile Glu Ala Leu
740 745 750

Gly His Cys Leu Arg Thr Tyr Arg Asp Tyr Lys Glu Ser Trp Arg Gly
755 760 765

Leu Gln Glu Arg Gly Met Ser Gln Asp Phe Ser Trp Glu His Ala Ala
770 775 780

Lys Leu Tyr Glu Asp Val Leu Val Lys Ala Lys Tyr Gln Trp
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Met Ser Ser Ala Val Ala Ser Ala
1 5

gcg tcc ttc ctc gcg ctc gcc tcc gcc tcc ccc ggg aga tca cgc agg 160
Ala Ser Phe Leu Ala Leu Ala Ser Ala Ser Pro Gly Arg Ser Arg Arg
10 15 20

cgg gcg agg gtg agc gcg ccg cca ccc cac gcc ggg gcc ggc agg ctg 208
Arg Ala Arg Val Ser Ala Pro Pro Pro His Ala Gly Ala Gly Arg Leu
25 30 35 40

cac tgg ccg ccg tgg ccg ccg cag cgc acg gct cgc gac gga ggt gtg 256
His Trp Pro Pro Trp Pro Pro Gln Arg Thr Ala Arg Asp Gly Gly Val
45 50 55

gcc gcg cgc gcc gcc ggg aag aag gac gcg agg gtc gac gac gac gcc 304
Ala Ala Arg Ala Ala Gly Lys Lys Asp Ala Arg Val Asp Asp Asp Ala
60 65 70

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gcg | tcc | gcg | agg | cag | ccc | cgc | gca | cgc | cgc | ggt | ggc | gcc | gcc | acc | aag | 352 |
| Ala | Ser | Ala | Arg | Gln | Pro | Arg | Ala | Arg | Arg | Gly | Gly | Ala | Ala | Thr | Lys | |
| 75 | | | | | | 80 | | | 85 | | | | | | | |
| gtc | gcg | gag | cgg | agg | gat | ccc | gtc | aag | acg | ctc | gat | cgc | gac | gcc | gcg | 400 |
| Val | Ala | Glu | Arg | Arg | Asp | Pro | Val | Lys | Thr | Leu | Asp | Arg | Asp | Ala | Ala | |
| 90 | | | | | | 95 | | | 100 | | | | | | | |
| gaa | ggt | ggc | gcg | ccg | gca | ccg | ccg | gca | ccg | agg | cag | gac | gcc | gcc | cgt | 448 |
| Glu | Gly | Gly | Ala | Pro | Ala | Pro | Pro | Ala | Pro | Arg | Gln | Asp | Ala | Ala | Arg | |
| 105 | | | | | 110 | | | 115 | | | 120 | | | | | |
| cca | ccg | agt | atg | aac | ggc | acg | ccg | gtg | aac | ggt | gag | aac | aaa | tct | acc | 496 |
| Pro | Pro | Ser | Met | Asn | Gly | Thr | Pro | Val | Asn | Gly | Glu | Asn | Lys | Ser | Thr | |
| | | | 125 | | | | | | 130 | | | 135 | | | | |
| ggc | ggc | ggc | ggc | gcg | acc | aaa | gac | agc | ggg | ctg | ccc | gca | ccc | gca | cgc | 544 |
| Gly | Gly | Gly | Gly | Ala | Thr | Lys | Asp | Ser | Gly | Leu | Pro | Ala | Pro | Ala | Arg | |
| | | | 140 | | | | | | 145 | | | 150 | | | | |
| gcg | ccc | cat | ccg | tcg | acc | cag | aac | aga | gta | cca | gtg | aac | ggt | gaa | aac | 592 |
| Ala | Pro | His | Pro | Ser | Thr | Gln | Asn | Arg | Val | Pro | Val | Asn | Gly | Glu | Asn | |
| 155 | | | | | | 160 | | | 165 | | | | | | | |
| aaa | gct | aac | gtc | gcc | tcg | ccg | ccg | acg | agc | ata | gcc | gag | gtc | gtg | gct | 640 |
| Lys | Ala | Asn | Val | Ala | Ser | Pro | Pro | Thr | Ser | Ile | Ala | Glu | Val | Val | Ala | |
| 170 | | | | | | 175 | | | 180 | | | | | | | |
| ccg | gat | tcc | gca | gct | acc | att | tcc | atc | agt | gac | aag | gcg | ccg | gag | tcc | 688 |
| Pro | Asp | Ser | Ala | Ala | Thr | Ile | Ser | Ile | Ser | Asp | Lys | Ala | Pro | Glu | Ser | |
| 185 | | | | | 190 | | | 195 | | | 200 | | | | | |
| gtt | gtc | cca | gcc | gag | aag | ccg | ccg | ccg | tcg | tcc | ggc | tca | aat | ttc | gtg | 736 |
| Val | Val | Pro | Ala | Glu | Lys | Pro | Pro | Pro | Ser | Ser | Gly | Ser | Asn | Phe | Val | |
| | | | 205 | | | | | | 210 | | | 215 | | | | |
| gtc | tcg | gct | tct | gct | ccc | agg | ctg | gac | att | gac | agc | gat | gtt | gaa | cct | 784 |
| Val | Ser | Ala | Ser | Ala | Pro | Arg | Leu | Asp | Ile | Asp | Ser | Asp | Val | Glu | Pro | |
| | | | 220 | | | | | | 225 | | | 230 | | | | |
| gaa | ctg | aag | aag | ggt | gcg | gtc | atc | gtc | gaa | gaa | gct | cca | aac | cca | aag | 832 |
| Glu | Leu | Lys | Lys | Gly | Ala | Val | Ile | Val | Glu | Glu | Ala | Pro | Asn | Pro | Lys | |
| 235 | | | | | | 240 | | | 245 | | | | | | | |
| gct | ctt | tcg | ccg | cct | gca | gcc | ccc | gct | gta | caa | gaa | gac | ctt | tgg | gac | 880 |
| Ala | Leu | Ser | Pro | Pro | Ala | Ala | Pro | Ala | Val | Gln | Glu | Asp | Leu | Trp | Asp | |
| 250 | | | | | | 255 | | | 260 | | | | | | | |
| ttc | aag | aaa | tac | att | ggc | ttc | gag | gag | ccc | gtg | gag | gcc | aag | gat | gat | 928 |
| Phe | Lys | Lys | Tyr | Ile | Gly | Phe | Glu | Glu | Pro | Val | Glu | Ala | Lys | Asp | Asp | |
| 265 | | | | | 270 | | | 275 | | | 280 | | | | | |
| ggc | tgg | gct | gtt | gca | gat | gat | gcg | ggc | tcc | ttt | gaa | cat | cac | cag | aac | 976 |
| Gly | Trp | Ala | Val | Ala | Asp | Asp | Ala | Gly | Ser | Phe | Glu | His | His | Gln | Asn | |
| | | | 285 | | | | | | 290 | | | 295 | | | | |

| | |
|---|------|
| cat gat tcc gga cct ttg gca ggg gag aac gtc atg aac gtg gtc gtc | 1024 |
| His Asp Ser Gly Pro Leu Ala Gly Glu Asn Val Met Asn Val Val Val | |
| 300 305 310 | |
| gtg gct gct gaa tgt tct ccc tgg tgc aaa aca ggt ggt ctt gga gat | 1072 |
| Val Ala Ala Glu Cys Ser Pro Trp Cys Lys Thr Gly Gly Leu Gly Asp | |
| 315 320 325 | |
| gtt gcc ggt gct ttg ccc aag gct ttg gcg aag aga gga cat cgt gtt | 1120 |
| Val Ala Gly Ala Leu Pro Lys Ala Leu Ala Lys Arg Gly His Arg Val | |
| 330 335 340 | |
| atg gtt gtg gta cca agg tat ggg gac tat gag gaa gcc tac gat gtc | 1168 |
| Met Val Val Val Pro Arg Tyr Gly Asp Tyr Glu Glu Ala Tyr Asp Val | |
| 345 350 355 360 | |
| gga gtc cga aaa tac tac aag gct gct gga cag gat atg gaa gtg aat | 1216 |
| Gly Val Arg Lys Tyr Tyr Lys Ala Ala Gly Gln Asp Met Glu Val Asn | |
| 365 370 375 | |
| tat ttc cat gct tat atc gat gga gtt gat ttt gtg ttc att gac gct | 1264 |
| Tyr Phe His Ala Tyr Ile Asp Gly Val Asp Phe Val Phe Ile Asp Ala | |
| 380 385 390 | |
| cct ctc ttc cga cac cgc cag gaa gac att tat ggg ggc agc aga cag | 1312 |
| Pro Leu Phe Arg His Arg Gln Glu Asp Ile Tyr Gly Gly Ser Arg Gln | |
| 395 400 405 | |
| gaa att atg aag cgc atg att ttg ttc tgc aag gcc gct gtc gag gtt | 1360 |
| Glu Ile Met Lys Arg Met Ile Leu Phe Cys Lys Ala Ala Val Glu Val | |
| 410 415 420 | |
| cct tgg cac gtt cca tgc ggc ggt gtc cct tat ggg gat gga aat ctg | 1408 |
| Pro Trp His Val Pro Cys Gly Gly Val Pro Tyr Gly Asp Gly Asn Leu | |
| 425 430 435 440 | |
| gtg ttt att gca aat gat tgg cac acg gca ctc ctg cct gtc tat ctg | 1456 |
| Val Phe Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro Val Tyr Leu | |
| 445 450 455 | |
| aaa gca tat tac agg gac cat ggt ttg atg cag tac act cgg tcc att | 1504 |
| Lys Ala Tyr Tyr Arg Asp His Gly Leu Met Gln Tyr Thr Arg Ser Ile | |
| 460 465 470 | |
| atg gtg ata cat aac atc gcg cac cag ggc cgt ggc cca gta gat gaa | 1552 |
| Met Val Ile His Asn Ile Ala His Gln Gly Arg Gly Pro Val Asp Glu | |
| 475 480 485 | |
| ttc ccg ttc acc gag ttg cct gag cac tac ctg gaa cac ttc aga ctg | 1600 |
| Phe Pro Phe Thr Glu Leu Pro Glu His Tyr Leu Glu His Phe Arg Leu | |
| 490 495 500 | |
| tac gac ccc gtg ggt ggt gag cac gcc aac tac ttc gcc gcc ggc ctg | 1648 |
| Tyr Asp Pro Val Gly Gly Glu His Ala Asn Tyr Phe Ala Ala Gly Leu | |
| 505 510 515 520 | |

| | | | | | | | | | | | | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| aag Lys | atg Met | gcg Ala | gac Asp | cag Gln 525 | gtt Val | gtc Val | gtg Val | gtg Val | agc Ser | ccc Pro | ggg Gly | tac Tyr | ctg Leu | tgg Trp | gag Glu 535 | 1696 |
| ctc Leu | aag Lys | acg Thr | gtg Val 540 | gag Glu | ggc Gly | ggc Gly | tgg Trp | ggg Gly 545 | ctt Leu | cac His | gac Asp | atc Ile | ata Ile 550 | cgg Arg | cag Gln | 1744 |
| aac Asn | gac Asp | tgg Trp 555 | aag Lys | acc Thr | cgc Arg | ggc Gly | atc Ile 560 | gtc Val | aac Asn | ggc Gly | atc Ile | gac Asp 565 | aac Asn | atg Met | gag Glu | 1792 |
| tgg Trp | aac Asn 570 | ccc Pro | gag Glu | gtg Val | gac Asp | gtc Val 575 | cac His | ctc Leu | aag Lys | tcg Ser | gac Asp 580 | ggc Gly | tac Tyr | acc Thr | aac Asn | 1840 |
| ttc Phe 585 | tcc Ser | ctg Leu | ggg Gly | acg Thr 590 | ctg Leu | gac Asp | tcc Ser | ggc Gly | aag Lys | cgg Arg 595 | cag Gln | tgc Cys | aag Lys | gag Glu | gcc Ala 600 | 1888 |
| ctg Leu | cag Gln | cgc Arg | gag Glu 605 | ctg Leu | ggc Gly | ctg Leu | cag Gln | gtc Val 610 | cgc Arg | gcc Ala | gac Asp | gtg Val | ccg Pro | ctg Leu 615 | ctc Leu | 1936 |
| ggc Gly | ttc Phe | atc Ile | ggc Gly 620 | cgc Arg | ctg Leu | gac Asp | ggg Gly | cag Gln 625 | aag Lys | ggc Gly | gtg Val | gag Glu | atc Ile 630 | atc Ile | gcg Ala | 1984 |
| gac Asp | gcc Ala | atg Met 635 | ccc Pro | tgg Trp | atc Ile | gtg Val 640 | agc Ser | cag Gln | gac Asp | gtg Val | cag Gln | ctg Leu 645 | gtc Val | atg Met | ctg Leu | 2032 |
| ggc Gly | acc Thr 650 | ggc Gly | cgc Arg | cac His | gac Asp | ctg Leu 655 | gag Glu | agc Ser | atg Met | ctg Leu | cgg Arg 660 | cac His | ttc Phe | gag Glu | cgg Arg | 2080 |
| gag Glu 665 | cac His | cac His | gac Asp | aag Lys 670 | gtg Val | cgc Arg | ggg Gly | tgg Trp | gtg Val | ggg Gly 675 | ttc Phe | tcc Ser | gtg Val | cgc Arg | ctg Leu 680 | 2128 |
| gcg Ala | cac His | cgg Arg | atc Ile 685 | acg Thr | gcg Ala | ggc Gly | gcc Ala | gac Asp 690 | gcg Ala | ctc Leu | ctc Leu | atg Met | ccc Pro | tcc Ser 695 | cgg Arg | 2176 |
| ttc Phe | gag Glu | ccg Pro | tgc Cys 700 | ggg Gly | ttg Leu | aac Asn | cag Gln | ctt Leu 705 | tac Tyr | gcc Ala | atg Met | gcc Ala 710 | tac Tyr | ggc Gly | acc Thr | 2224 |
| gtc Val | ccc Pro | gtc Val 715 | gtg Val | cac His | gcc Ala | gtc Val | ggc Gly 720 | ggg Gly | gtg Val | agg Arg | gac Asp | acc Thr 725 | gtg Val | ccg Pro | ccg Pro | 2272 |
| ttc Phe 730 | gac Asp | ccc Pro | ttc Phe | aac Asn | cac His | tcc Ser 735 | ggc Gly | ctc Leu | ggg Gly | tgg Trp | acg Thr 740 | ttc Phe | gac Asp | cgc Arg | gcc Ala | 2320 |

$$f_{\alpha} = \frac{1}{(2\pi)^n} \int_{\mathbb{R}^n} f(x) e^{-ix \cdot \alpha} dx$$

cgg gac tac aag gag agc tgg agg ggc ctc cag gag cgc ggc atg tcg 2416
Arg Asp Tyr Lys Glu Ser Trp Arg Gly Leu Gln Glu Arg Gly Met Ser
765 770 775

cag gac ttc agc tgg gag cat gcc gcc aag ctc tac gag gac gtc ctc 2464
Gln Asp Phe Ser Trp Glu His Ala Ala Lys Leu Tyr Glu Asp Val Leu
780 785 790

ctc aag gcc aag tac cag tgg tgaacgctag ctgctagccg ctccagcccc 2515
Leu Lys Ala Lys Tyr Gln Trp
795

gcatgcgtgc atgcatgaga ggggtggaact gcgcattgcg cccgcaggaa cgtgccatcc 2575

ttctcgatgg gagcgccggc atccgcgagg tgcagtgaca tgagaggtgt gtgtggttga 2635

gacgctgatt ccgatctcga tctgggtccgt agcagagtag agcggacgta gggaagcgct 2695

ccttgttgca ggtatatggg aatgttgtca acttggtatt gtagtttgct atgttgtatg 2755

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cacatgaaaa aaaaaaaaaa aaaaaaa 2842

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Pro His Ala Gly Ala Gly Arg Leu His Trp Pro Pro Trp Pro Pro Gln
35 40 45

Arg Thr Ala Arg Asp Gly Gly Val Ala Ala Arg Ala Ala Gly Lys Lys
50 55 60

Asp Ala Arg Val Asp Asp Asp Ala Ala Ser Ala Arg Gln Pro Arg Ala
65 70 75 80

Arg Arg Gly Gly Ala Ala Thr Lys Val Ala Glu Arg Arg Asp Pro Val
85 90 95

Lys Thr Leu Asp Arg Asp Ala Ala Glu Gly Gly Ala Pro Ala Pro Pro
100 105 110

Ala Pro Arg Gln Asp Ala Ala Arg Pro Pro Ser Met Asn Gly Thr Pro
115 120 125

Val Asn Gly Glu Asn Lys Ser Thr Gly Gly Gly Gly Ala Thr Lys Asp
130 135 140

Ser Gly Leu Pro Ala Pro Ala Arg Ala Pro His Pro Ser Thr Gln Asn
145 150 155 160

Arg Val Pro Val Asn Gly Glu Asn Lys Ala Asn Val Ala Ser Pro Pro
165 170 175

Thr Ser Ile Ala Glu Val Val Ala Pro Asp Ser Ala Ala Thr Ile Ser
180 185 190

Ile Ser Asp Lys Ala Pro Glu Ser Val Val Pro Ala Glu Lys Pro Pro
195 200 205

Pro Ser Ser Gly Ser Asn Phe Val Val Ser Ala Ser Ala Pro Arg Leu
210 215 220

Asp Ile Asp Ser Asp Val Glu Pro Glu Leu Lys Lys Gly Ala Val Ile
225 230 235 240

Val Glu Glu Ala Pro Asn Pro Lys Ala Leu Ser Pro Pro Ala Ala Pro
245 250 255

Ala Val Gln Glu Asp Leu Trp Asp Phe Lys Lys Tyr Ile Gly Phe Glu
260 265 270

Glu Pro Val Glu Ala Lys Asp Asp Gly Trp Ala Val Ala Asp Asp Ala
275 280 285

Gly Ser Phe Glu His His Gln Asn His Asp Ser Gly Pro Leu Ala Gly
290 295 300

Glu Asn Val Met Asn Val Val Val Val Ala Ala Glu Cys Ser Pro Trp
305 310 315 320

Cys Lys Thr Gly Gly Leu Gly Asp Val Ala Gly Ala Leu Pro Lys Ala
325 330 335

Leu Ala Lys Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr Gly
340 345 350

Asp Tyr Glu Glu Ala Tyr Asp Val Gly Val Arg Lys Tyr Tyr Lys Ala
355 360 365

Ala Gly Gln Asp Met Glu Val Asn Tyr Phe His Ala Tyr Ile Asp Gly
370 375 380

Val Asp Phe Val Phe Ile Asp Ala Pro Leu Phe Arg His Arg Gln Glu
385 390 395 400

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Tyr | Gly | Gly | Ser | Arg | Gln | Glu | Ile | Met | Lys | Arg | Met | Ile | Leu |
| 405 | | | | | | | | 410 | | | | 415 | | | |
| Phe | Cys | Lys | Ala | Ala | Val | Glu | Val | Pro | Trp | His | Val | Pro | Cys | Gly | Gly |
| 420 | | | | | | | | 425 | | | | 430 | | | |
| Val | Pro | Tyr | Gly | Asp | Gly | Asn | Leu | Val | Phe | Ile | Ala | Asn | Asp | Trp | His |
| 435 | | | | | | | | 440 | | | | 445 | | | |
| Thr | Ala | Leu | Leu | Pro | Val | Tyr | Leu | Lys | Ala | Tyr | Tyr | Arg | Asp | His | Gly |
| 450 | | | | | | | | 455 | | | | 460 | | | |
| Leu | Met | Gln | Tyr | Thr | Arg | Ser | Ile | Met | Val | Ile | His | Asn | Ile | Ala | His |
| 465 | | | | | | | | 470 | | | | 475 | | | |
| Gln | Gly | Arg | Gly | Pro | Val | Asp | Glu | Phe | Pro | Phe | Thr | Glu | Leu | Pro | Glu |
| 485 | | | | | | | | 490 | | | | 495 | | | |
| His | Tyr | Leu | Glu | His | Phe | Arg | Leu | Tyr | Asp | Pro | Val | Gly | Gly | Glu | His |
| 500 | | | | | | | | 505 | | | | 510 | | | |
| Ala | Asn | Tyr | Phe | Ala | Ala | Gly | Leu | Lys | Met | Ala | Asp | Gln | Val | Val | Val |
| 515 | | | | | | | | 520 | | | | 525 | | | |
| Val | Ser | Pro | Gly | Tyr | Leu | Trp | Glu | Leu | Lys | Thr | Val | Glu | Gly | Gly | Trp |
| 530 | | | | | | | | 535 | | | | 540 | | | |
| Gly | Leu | His | Asp | Ile | Ile | Arg | Gln | Asn | Asp | Trp | Lys | Thr | Arg | Gly | Ile |
| 545 | | | | | | | | 550 | | | | 555 | | | |
| Val | Asn | Gly | Ile | Asp | Asn | Met | Glu | Trp | Asn | Pro | Glu | Val | Asp | Val | His |
| 565 | | | | | | | | 570 | | | | 575 | | | |
| Leu | Lys | Ser | Asp | Gly | Tyr | Thr | Asn | Phe | Ser | Leu | Gly | Thr | Leu | Asp | Ser |
| 580 | | | | | | | | 585 | | | | 590 | | | |
| Gly | Lys | Arg | Gln | Cys | Lys | Glu | Ala | Leu | Gln | Arg | Glu | Leu | Gly | Leu | Gln |
| 595 | | | | | | | | 600 | | | | 605 | | | |
| Val | Arg | Ala | Asp | Val | Pro | Leu | Leu | Gly | Phe | Ile | Gly | Arg | Leu | Asp | Gly |
| 610 | | | | | | | | 615 | | | | 620 | | | |
| Gln | Lys | Gly | Val | Glu | Ile | Ile | Ala | Asp | Ala | Met | Pro | Trp | Ile | Val | Ser |
| 625 | | | | | | | | 630 | | | | 635 | | | |
| Gln | Asp | Val | Gln | Leu | Val | Met | Leu | Gly | Thr | Gly | Arg | His | Asp | Leu | Glu |
| 645 | | | | | | | | 650 | | | | 655 | | | |
| Ser | Met | Leu | Arg | His | Phe | Glu | Arg | Glu | His | His | Asp | Lys | Val | Arg | Gly |
| 660 | | | | | | | | 665 | | | | 670 | | | |
| Trp | Val | Gly | Phe | Ser | Val | Arg | Leu | Ala | His | Arg | Ile | Thr | Ala | Gly | Ala |
| 675 | | | | | | | | 680 | | | | 685 | | | |

Asp Ala Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln
690 695 700

Leu Tyr Ala Met Ala Tyr Gly Thr Val Pro Val Val His Ala Val Gly
705 710 715 720

Gly Val Arg Asp Thr Val Pro Pro Phe Asp Pro Phe Asn His Ser Gly
725 730 735

Leu Gly Trp Thr Phe Asp Arg Ala Glu Ala His Lys Leu Ile Glu Ala
740 745 750

Leu Gly His Cys Leu Arg Thr Tyr Arg Asp Tyr Lys Glu Ser Trp Arg
755 760 765

Gly Leu Gln Glu Arg Gly Met Ser Gln Asp Phe Ser Trp Glu His Ala
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Ala Lys Leu Tyr Glu Asp Val Leu Leu Lys Ala Lys Tyr Gln Trp
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Pro Ala Glu Lys Thr Pro Pro Ser Ser Gly Ser Asn Phe Glu Ser Ser
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gcc tct gct ccc ggg tct gac act gtc agc gac gtg gaa caa gaa ctg 96
Ala Ser Ala Pro Gly Ser Asp Thr Val Ser Asp Val Glu Gln Glu Leu
20 25 30

aag aag ggt gcg gtc gtt gtc gaa gaa gct cca aag cca aag gct ctt 144
Lys Lys Gly Ala Val Val Val Glu Glu Ala Pro Lys Pro Lys Ala Leu
35 40 45

tcg ccg cct gca gcc ccc gct gta caa gaa gac ctt tgg gat ttc aag 192
Ser Pro Pro Ala Ala Pro Ala Val Gln Glu Asp Leu Trp Asp Phe Lys
50 55 60

aaa tac att ggt ttc gag gag ccc gtg gag gcc aag gat gat ggc cgg 240
Lys Tyr Ile Gly Phe Glu Glu Pro Val Glu Ala Lys Asp Asp Gly Arg
65 70 75 80

gct gtc gca gat gat gcg ggc tcc ttt gaa cac cac cag aat cac gac 288
Ala Val Ala Asp Asp Ala Gly Ser Phe Glu His His Gln Asn His Asp
85 90 95

| | |
|---|-----|
| tcc gga cct ttg gca ggg gag aat gtc atg aac gtg gtc gtc gtg gct | 336 |
| Ser Gly Pro Leu Ala Gly Glu Asn Val Met Asn Val Val Val Val Ala | |
| 100 105 110 | |
| gct gag tgt tct ccc tgg tgc aaa aca ggt ggt ctg gga gat gtt gcg | 384 |
| Ala Glu Cys Ser Pro Trp Cys Lys Thr Gly Gly Leu Gly Asp Val Ala | |
| 115 120 125 | |
| ggt gct ctg ccc aag gct ttg gca aag aga gga cat cgt gtt atg gtt | 432 |
| Gly Ala Leu Pro Lys Ala Leu Ala Lys Arg Gly His Arg Val Met Val | |
| 130 135 140 | |
| gtg gta cca agg tat ggg gac tat gaa gaa cct acg gat gtc gga gtc | 480 |
| Val Val Pro Arg Tyr Gly Asp Tyr Glu Glu Pro Thr Asp Val Gly Val | |
| 145 150 155 160 | |
| cga aaa tac tac aag gct gct gga cag gat atg gaa gtg aat tat ttc | 528 |
| Arg Lys Tyr Tyr Lys Ala Ala Gly Gln Asp Met Glu Val Asn Tyr Phe | |
| 165 170 175 | |
| cat gct tat atc gat gga gtt gat ttt gtg ttc att gac gct cct ctc | 576 |
| His Ala Tyr Ile Asp Gly Val Asp Phe Val Phe Ile Asp Ala Pro Leu | |
| 180 185 190 | |
| ttc cga cac cga gag gaa gac att tat ggg ggc agc aga cag gaa att | 624 |
| Phe Arg His Arg Glu Glu Asp Ile Tyr Gly Gly Ser Arg Gln Glu Ile | |
| 195 200 205 | |
| atg aag cgc atg att ttg ttc tgc aag gcc gct gtt gag gtt cca tgg | 672 |
| Met Lys Arg Met Ile Leu Phe Cys Lys Ala Ala Val Glu Val Pro Trp | |
| 210 215 220 | |
| cac gtt cca tgc ggc ggt gtc cct tat ggg gat gga aat ctg gtg ttt | 720 |
| His Val Pro Cys Gly Gly Val Pro Tyr Gly Asp Gly Asn Leu Val Phe | |
| 225 230 235 240 | |
| att gca aat gat tgg cac acg gca ctc ctg cct gtc tat ctg aaa gca | 768 |
| Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro Val Tyr Leu Lys Ala | |
| 245 250 255 | |
| tat tac agg gac cat ggt ttg atg cag tac act cgg tcc att atg gtg | 816 |
| Tyr Tyr Arg Asp His Gly Leu Met Gln Tyr Thr Arg Ser Ile Met Val | |
| 260 265 270 | |
| ata cat aac atc gct cac cag ggc cgt ggc cct gta gat gaa ttc ccg | 864 |
| Ile His Asn Ile Ala His Gln Gly Arg Gly Pro Val Asp Glu Phe Pro | |
| 275 280 285 | |
| ttc acc gag ttg cct gag cac tac ctg gaa cac ttc aga ctg tac gac | 912 |
| Phe Thr Glu Leu Pro Glu His Tyr Leu Glu His Phe Arg Leu Tyr Asp | |
| 290 295 300 | |
| ccc gtg ggt ggt gaa cac gcc aac tac ttc gcc gcc ggc ctg aag atg | 960 |
| Pro Val Gly Gly Glu His Ala Asn Tyr Phe Ala Ala Gly Leu Lys Met | |
| 305 310 315 320 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| gcg | gac | cag | gtt | gtc | gtg | gtg | agc | ccc | ggg | tac | ctg | tgg | gag | ctg | aag | 1008 |
| Ala | Asp | Gln | Val | Val | Val | Val | Ser | Pro | Gly | Tyr | Leu | Trp | Glu | Leu | Lys | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| acg | gtg | gag | ggc | ggc | tgg | ggg | ctt | cac | gac | atc | ata | cgg | cag | aac | gac | 1056 |
| Thr | Val | Glu | Gly | Gly | Trp | Gly | Leu | His | Asp | Ile | Ile | Arg | Gln | Asn | Asp | |
| | | | | 340 | | | | | 345 | | | | | 350 | | |
| tgg | aag | acc | cgc | ggc | atc | gtc | aac | ggc | atc | gac | aac | atg | gag | tgg | aac | 1104 |
| Trp | Lys | Thr | Arg | Gly | Ile | Val | Asn | Gly | Ile | Asp | Asn | Met | Glu | Trp | Asn | |
| | | | | 355 | | | | | 360 | | | | | 365 | | |
| ccc | gag | gtg | gac | gcc | cac | ctc | aag | tcg | gac | ggc | tac | acc | aac | ttc | tcc | 1152 |
| Pro | Glu | Val | Asp | Ala | His | Leu | Lys | Ser | Asp | Gly | Tyr | Thr | Asn | Phe | Ser | |
| | | | | 370 | | | | | 375 | | | | | 380 | | |
| ctg | agg | acg | ctg | gac | tcc | ggc | aag | cgg | cag | tgc | aag | gag | gcc | ctg | cag | 1200 |
| Leu | Arg | Thr | Leu | Asp | Ser | Gly | Lys | Arg | Gln | Cys | Lys | Glu | Ala | Leu | Gln | |
| | | | | 385 | | | | | 390 | | | | | 395 | | |
| cgc | gag | ctg | ggc | ctg | cag | gtc | cgc | gcc | gac | gtg | ccg | ctg | ctc | ggc | ttc | 1248 |
| Arg | Glu | Leu | Gly | Leu | Gln | Val | Arg | Ala | Asp | Val | Pro | Leu | Leu | Gly | Phe | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| atc | ggc | cgc | ctg | gac | ggg | cag | aag | ggc | gtg | gag | atc | atc | gcg | gac | gcc | 1296 |
| Ile | Gly | Arg | Leu | Asp | Gly | Gln | Lys | Gly | Val | Glu | Ile | Ile | Ala | Asp | Ala | |
| | | | | 420 | | | | | 425 | | | | | 430 | | |
| atg | ccc | tgg | atc | gtg | agc | cag | gac | gtg | cag | ctg | gtg | atg | ctg | ggc | acc | 1344 |
| Met | Pro | Trp | Ile | Val | Ser | Gln | Asp | Val | Gln | Leu | Val | Met | Leu | Gly | Thr | |
| | | | | 435 | | | | | 440 | | | | | 445 | | |
| ggg | cgc | cac | gac | ctg | gag | agc | atg | ctg | cag | cac | ttc | gag | cgg | gag | cac | 1392 |
| Gly | Arg | His | Asp | Leu | Glu | Ser | Met | Leu | Gln | His | Phe | Glu | Arg | Glu | His | |
| | | | | 450 | | | | | 455 | | | | | 460 | | |
| cac | gac | aag | gtg | cgc | ggg | tgg | gtg | ggg | ttc | tcc | gtg | cgc | ctg | gcg | cac | 1440 |
| His | Asp | Lys | Val | Arg | Gly | Trp | Val | Gly | Phe | Ser | Val | Arg | Leu | Ala | His | |
| | | | | 465 | | | | | 470 | | | | | 475 | | |
| cgg | atc | acg | gcg | ggg | gcg | gac | gcg | ctc | ctc | atg | ccc | tcc | cgg | ttc | gtg | 1488 |
| Arg | Ile | Thr | Ala | Gly | Ala | Asp | Ala | Leu | Leu | Met | Pro | Ser | Arg | Phe | Val | |
| | | | | 485 | | | | | 490 | | | | | 495 | | |
| ccg | tgc | ggg | ctg | aac | cag | ctc | tac | gcc | atg | gcc | tac | ggc | acc | gtc | ccc | 1536 |
| Pro | Cys | Gly | Leu | Asn | Gln | Leu | Tyr | Ala | Met | Ala | Tyr | Gly | Thr | Val | Pro | |
| | | | | 500 | | | | | 505 | | | | | 510 | | |
| gtc | gtg | cac | gcc | gtc | ggc | ggc | ctc | agg | gac | acc | gtg | ccg | ccg | ttc | gac | 1584 |
| Val | Val | His | Ala | Val | Gly | Gly | Leu | Arg | Asp | Thr | Val | Pro | Pro | Phe | Asp | |
| | | | | 515 | | | | | 520 | | | | | 525 | | |
| ccc | ttc | aac | cac | tcc | ggg | ctc | ggg | tgg | acg | ttc | gac | cgc | gcc | gag | gcg | 1632 |
| Pro | Phe | Asn | His | Ser | Gly | Leu | Gly | Trp | Thr | Phe | Asp | Arg | Ala | Glu | Ala | |
| | | | | 530 | | | | | 535 | | | | | 540 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ala | Leu | Pro | Lys | Ala | Leu | Ala | Lys | Arg | Gly | His | Arg | Val | Met | Val |
| 130 | | | | | | 135 | | | | | 140 | | | | |
| Val | Val | Pro | Arg | Tyr | Gly | Asp | Tyr | Glu | Glu | Pro | Thr | Asp | Val | Gly | Val |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Arg | Lys | Tyr | Tyr | Lys | Ala | Ala | Gly | Gln | Asp | Met | Glu | Val | Asn | Tyr | Phe |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| His | Ala | Tyr | Ile | Asp | Gly | Val | Asp | Phe | Val | Phe | Ile | Asp | Ala | Pro | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Phe | Arg | His | Arg | Glu | Glu | Asp | Ile | Tyr | Gly | Gly | Ser | Arg | Gln | Glu | Ile |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Met | Lys | Arg | Met | Ile | Leu | Phe | Cys | Lys | Ala | Ala | Val | Glu | Val | Pro | Trp |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| His | Val | Pro | Cys | Gly | Gly | Val | Pro | Tyr | Gly | Asp | Gly | Asn | Leu | Val | Phe |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Ile | Ala | Asn | Asp | Trp | His | Thr | Ala | Leu | Leu | Pro | Val | Tyr | Leu | Lys | Ala |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Tyr | Tyr | Arg | Asp | His | Gly | Leu | Met | Gln | Tyr | Thr | Arg | Ser | Ile | Met | Val |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ile | His | Asn | Ile | Ala | His | Gln | Gly | Arg | Gly | Pro | Val | Asp | Glu | Phe | Pro |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Phe | Thr | Glu | Leu | Pro | Glu | His | Tyr | Leu | Glu | His | Phe | Arg | Leu | Tyr | Asp |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Pro | Val | Gly | Gly | Glu | His | Ala | Asn | Tyr | Phe | Ala | Ala | Gly | Leu | Lys | Met |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Ala | Asp | Gln | Val | Val | Val | Val | Ser | Pro | Gly | Tyr | Leu | Trp | Glu | Leu | Lys |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Thr | Val | Glu | Gly | Gly | Trp | Gly | Leu | His | Asp | Ile | Ile | Arg | Gln | Asn | Asp |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Trp | Lys | Thr | Arg | Gly | Ile | Val | Asn | Gly | Ile | Asp | Asn | Met | Glu | Trp | Asn |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Pro | Glu | Val | Asp | Ala | His | Leu | Lys | Ser | Asp | Gly | Tyr | Thr | Asn | Phe | Ser |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Leu | Arg | Thr | Leu | Asp | Ser | Gly | Lys | Arg | Gln | Cys | Lys | Glu | Ala | Leu | Gln |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Arg | Glu | Leu | Gly | Leu | Gln | Val | Arg | Ala | Asp | Val | Pro | Leu | Leu | Gly | Phe |
| | | | | 405 | | | | | 410 | | | | | 415 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gcc | ggc | cgc | ggc | ggc | ctc | acg | cag | cct | ttt | ttg | atg | aat | ggc | aga | ttt | 148 |
| Ala | Gly | Arg | Gly | Gly | Leu | Thr | Gln | Pro | Phe | Leu | Met | Asn | Gly | Arg | Phe | |
| 25 | | | | | 30 | | | | | 35 | | | | | 40 | |
| act | cga | agc | agg | acc | ctt | cga | tgc | atg | gta | gca | agt | tca | gat | cct | cct | 196 |
| Thr | Arg | Ser | Arg | Thr | Leu | Arg | Cys | Met | Val | Ala | Ser | Ser | Asp | Pro | Pro | |
| | | | | 45 | | | | | 50 | | | | | 55 | | |
| aat | agg | aaa | tca | aga | agg | atg | gta | cca | cct | cag | gtt | aaa | gtc | att | tct | 244 |
| Asn | Arg | Lys | Ser | Arg | Arg | Met | Val | Pro | Pro | Gln | Val | Lys | Val | Ile | Ser | |
| | | | 60 | | | | | 65 | | | | | 70 | | | |
| tct | aga | gga | tat | acg | aca | aga | ctc | att | gtt | gaa | cca | agc | aac | gag | aat | 292 |
| Ser | Arg | Gly | Tyr | Thr | Thr | Arg | Leu | Ile | Val | Glu | Pro | Ser | Asn | Glu | Asn | |
| | | 75 | | | | | 80 | | | | | 85 | | | | |
| aca | gaa | cac | aat | aat | cgg | gat | gaa | gaa | act | ctt | gat | aca | tac | aat | gcg | 340 |
| Thr | Glu | His | Asn | Asn | Arg | Asp | Glu | Glu | Thr | Leu | Asp | Thr | Tyr | Asn | Ala | |
| | 90 | | | | | 95 | | | | | 100 | | | | | |
| cta | tta | agt | acc | gag | aca | gca | gaa | tgg | aca | gat | aat | aga | gaa | gcc | gag | 388 |
| Leu | Leu | Ser | Thr | Glu | Thr | Ala | Glu | Trp | Thr | Asp | Asn | Arg | Glu | Ala | Glu | |
| 105 | | | | 110 | | | | | | 115 | | | | | 120 | |
| act | gct | aaa | gcg | gac | tcg | tcg | caa | aat | gct | tta | agc | agt | tct | ata | att | 436 |
| Thr | Ala | Lys | Ala | Asp | Ser | Ser | Gln | Asn | Ala | Leu | Ser | Ser | Ser | Ile | Ile | |
| | | | 125 | | | | | | 130 | | | | | 135 | | |
| ggg | gaa | gtg | gat | gtg | gcg | gat | gaa | gat | ata | ctt | gcg | gct | gat | ctg | aca | 484 |
| Gly | Glu | Val | Asp | Val | Ala | Asp | Glu | Asp | Ile | Leu | Ala | Ala | Asp | Leu | Thr | |
| | | | 140 | | | | | 145 | | | | | 150 | | | |
| gtg | tat | tca | ttg | agc | agt | gta | atg | aag | aag | gaa | gtg | gat | gca | gcg | gac | 532 |
| Val | Tyr | Ser | Leu | Ser | Ser | Val | Met | Lys | Lys | Glu | Val | Asp | Ala | Ala | Asp | |
| | | 155 | | | | | 160 | | | | | 165 | | | | |
| aaa | gct | aga | gtt | aaa | gaa | gac | gca | ttt | gag | ctg | gat | ttg | cca | gca | act | 580 |
| Lys | Ala | Arg | Val | Lys | Glu | Asp | Ala | Phe | Glu | Leu | Asp | Leu | Pro | Ala | Thr | |
| | 170 | | | | | 175 | | | | | 180 | | | | | |
| aca | ttg | aga | agt | gtg | ata | gta | gat | gtg | atg | gat | cat | aat | ggg | act | gta | 628 |
| Thr | Leu | Arg | Ser | Val | Ile | Val | Asp | Val | Met | Asp | His | Asn | Gly | Thr | Val | |
| 185 | | | | 190 | | | | | | 195 | | | | | 200 | |
| caa | gag | aca | ttg | aga | agt | gtg | ata | gta | gat | gtg | atg | gat | cat | aat | ggg | 676 |
| Gln | Glu | Thr | Leu | Arg | Ser | Val | Ile | Val | Asp | Val | Met | Asp | His | Asn | Gly | |
| | | | 205 | | | | | | 210 | | | | | 215 | | |
| act | gta | caa | gag | aca | ttg | aga | agt | gtg | ata | gta | gat | gtg | atg | gat | gat | 724 |
| Thr | Val | Gln | Glu | Thr | Leu | Arg | Ser | Val | Ile | Val | Asp | Val | Met | Asp | Asp | |
| | | | 220 | | | | | 225 | | | | | 230 | | | |
| gcg | gcg | gac | aaa | gct | aga | gtt | gaa | gaa | gac | gta | ttt | gag | | | | |

| | |
|---|------|
| tca gga aat att tca agc agt gcg acg acc gtg gaa cta gat gcg gtt Ser Gly Asn Ile Ser Ser Ser Ala Thr Thr Val Glu Leu Asp Ala Val 250 255 260 | 820 |
| gac gaa gtc ggg cct gtt caa gac aaa ttt gag gcg acc tca tca gga Asp Glu Val Gly Pro Val Gln Asp Lys Phe Glu Ala Thr Ser Ser Gly 265 270 275 280 | 868 |
| aat gtt tca aac agt gca acg gta cgg gaa gtg gat gca agt gat gaa Asn Val Ser Asn Ser Ala Thr Val Arg Glu Val Asp Ala Ser Asp Glu 285 290 295 | 916 |
| gct ggg aat gat caa ggc ata ttt aga gca gat ttg tca gga aat gtt Ala Gly Asn Asp Gln Gly Ile Phe Arg Ala Asp Leu Ser Gly Asn Val 300 305 310 | 964 |
| ttt tca agc agt aca aca gtg gaa gtg ggt gca gtg gat gaa gct ggg Phe Ser Ser Ser Thr Thr Val Glu Val Gly Ala Val Asp Glu Ala Gly 315 320 325 | 1012 |
| tct ata aag gac agg ttt gag acg gat tcg tca gga aat gtt tca aca Ser Ile Lys Asp Arg Phe Glu Thr Asp Ser Ser Gly Asn Val Ser Thr 330 335 340 | 1060 |
| agt gcg ccg atg tgg gat gca att gat gaa acc gtg gct gat caa gac Ser Ala Pro Met Trp Asp Ala Ile Asp Glu Thr Val Ala Asp Gln Asp 345 350 355 360 | 1108 |
| aca ttt gag gcg gat ttg tcg gga aat gct tca agc tgc gca aca tac Thr Phe Glu Ala Asp Leu Ser Gly Asn Ala Ser Ser Cys Ala Thr Tyr 365 370 375 | 1156 |
| aga gaa gtg gat gat gtg gtg gat gaa act aga tca gaa gag gaa aca Arg Glu Val Asp Asp Val Val Asp Glu Thr Arg Ser Glu Glu Glu Thr 380 385 390 | 1204 |
| ttt gca atg gat ttg ttt gca agt gaa tca ggc cat gag aaa cat atg Phe Ala Met Asp Leu Phe Ala Ser Glu Ser Gly His Glu Lys His Met 395 400 405 | 1252 |
| gca gtg gat tat gtg ggt gaa gct acc gat gaa gaa gag act tac caa Ala Val Asp Tyr Val Gly Glu Ala Thr Asp Glu Glu Glu Thr Tyr Gln 410 415 420 | 1300 |
| cag caa tat cca gta ccg tct tca ttc tct atg tgg gac aag gct att Gln Gln Tyr Pro Val Pro Ser Ser Phe Ser Met Trp Asp Lys Ala Ile 425 430 435 440 | 1348 |
| gct aaa aca ggt gta agt ttg aat cct gag ctg cga ctt gtc agg gtt Ala Lys Thr Gly Val Ser Leu Asn Pro Glu Leu Arg Leu Val Arg Val 445 450 455 | 1396 |
| gaa gaa caa ggc aaa gta aat ttt agt gat aaa aaa gac ctg tca att Glu Glu Gln Gly Lys Val Asn Phe Ser Asp Lys Lys Asp Leu Ser Ile 460 465 470 | 1444 |

| | |
|---|------|
| gat gat tta cca gga caa aac caa tcg atc att ggt tcc tat aaa caa | 1492 |
| Asp Asp Leu Pro Gly Gln Asn Gln Ser Ile Ile Gly Ser Tyr Lys Gln | |
| 475 480 485 | |
| gat aaa tca att gct gat gtt gcg gga ccg acc caa tca att ttt ggt | 1540 |
| Asp Lys Ser Ile Ala Asp Val Ala Gly Pro Thr Gln Ser Ile Phe Gly | |
| 490 495 500 | |
| tct agt aaa caa cac cgg tca att gtt gct ttc ccc aaa caa aac cag | 1588 |
| Ser Ser Lys Gln His Arg Ser Ile Val Ala Phe Pro Lys Gln Asn Gln | |
| 505 510 515 520 | |
| tca att gtt agt gtc act gag caa aag cag tcc ata gtt gga ttc cgt | 1636 |
| Ser Ile Val Ser Val Thr Glu Gln Lys Gln Ser Ile Val Gly Phe Arg | |
| 525 530 535 | |
| agt caa gat ctt tcg gct gtt agt ctc cct aaa caa aac gta cca att | 1684 |
| Ser Gln Asp Leu Ser Ala Val Ser Leu Pro Lys Gln Asn Val Pro Ile | |
| 540 545 550 | |
| gtt ggt acg tcg aga gag ggt caa aca aag caa gtt cct gtt gtt gat | 1732 |
| Val Gly Thr Ser Arg Glu Gly Gln Thr Lys Gln Val Pro Val Val Asp | |
| 555 560 565 | |
| aga cag gat gca ttg tat gtg aat gga ctg gaa gct aag gag gga gat | 1780 |
| Arg Gln Asp Ala Leu Tyr Val Asn Gly Leu Glu Ala Lys Glu Gly Asp | |
| 570 575 580 | |
| cac aca tcc gag aaa act gat gag gat gcg ctt cat gta aag ttt aat | 1828 |
| His Thr Ser Glu Lys Thr Asp Glu Asp Ala Leu His Val Lys Phe Asn | |
| 585 590 595 600 | |
| gtt gac aat gtg ttg cgg aag cat cag gca gat aga acc caa gca gtg | 1876 |
| Val Asp Asn Val Leu Arg Lys His Gln Ala Asp Arg Thr Gln Ala Val | |
| 605 610 615 | |
| gaa aag aaa act tgg aag aaa gtt gat gag gaa cat ctt tac atg act | 1924 |
| Glu Lys Lys Thr Trp Lys Lys Val Asp Glu Glu His Leu Tyr Met Thr | |
| 620 625 630 | |
| gaa cat cag aaa cgt gct gcc gaa gga cag atg gta gtt aac gag gat | 1972 |
| Glu His Gln Lys Arg Ala Ala Glu Gly Gln Met Val Val Asn Glu Asp | |
| 635 640 645 | |
| gag ctt tct ata act gaa att gga atg ggg aga ggt gat aaa att cag | 2020 |
| Glu Leu Ser Ile Thr Glu Ile Gly Met Gly Arg Gly Asp Lys Ile Gln | |
| 650 655 660 | |
| cat gtg ctt tct gag gaa gag ctt tca tgg tct gaa gat gaa gtg cag | 2068 |
| His Val Leu Ser Glu Glu Glu Leu Ser Trp Ser Glu Asp Glu Val Gln | |
| 665 670 675 680 | |
| tta att gag gat gat gga caa tat gaa gtt gac gag acc tct gtg tcc | 2116 |
| Leu Ile Glu Asp Asp Gly Gln Tyr Glu Val Asp Glu Thr Ser Val Ser | |
| 685 690 695 | |

| | |
|---|------|
| gtt aac gtt gaa caa gat atc cag ggg tca cca cag gat gtt gtg gat Val Asn Val Glu Gln Asp Ile Gln Gly Ser Pro Gln Asp Val Val Asp 700 705 710 | 2164 |
| ccg caa gca cta aag gtg atg ctg caa gaa ctc gct gag aaa aat tat Pro Gln Ala Leu Lys Val Met Leu Gln Glu Leu Ala Glu Lys Asn Tyr 715 720 725 | 2212 |
| tcg atg agg aac aag ctg ttt gtt ttt cca gag gta gtg aaa gct gat Ser Met Arg Asn Lys Leu Phe Val Phe Pro Glu Val Val Lys Ala Asp 730 735 740 | 2260 |
| tca gtt att gat ctt tat tta aat cgt gac cta aca gct ttg gcg aat Ser Val Ile Asp Leu Tyr Leu Asn Arg Asp Leu Thr Ala Leu Ala Asn 745 750 755 760 | 2308 |
| gaa ccc gat gtc gtc atc aaa gga gca ttc aat ggt tgg aaa tgg agg Glu Pro Asp Val Val Ile Lys Gly Ala Phe Asn Gly Trp Lys Trp Arg 765 770 775 | 2356 |
| ctt ttc act gaa aga ttg cac aag agt gac ctt gga ggg gtt tgg tgg Leu Phe Thr Glu Arg Leu His Lys Ser Asp Leu Gly Gly Val Trp Trp 780 785 790 | 2404 |
| tct tgc aaa ctg tac ata ccc aag gag gcc tac aga tta gac ttt gtg Ser Cys Lys Leu Tyr Ile Pro Lys Glu Ala Tyr Arg Leu Asp Phe Val 795 800 805 | 2452 |
| ttc ttc aac ggt cgc acg gtc tat gag aac aat ggc aac aat gat ttc Phe Phe Asn Gly Arg Thr Val Tyr Glu Asn Asn Gly Asn Asn Asp Phe 810 815 820 | 2500 |
| tgt ata gga ata gaa ggc act atg aat gaa gat ctg ttt gag gat ttc Cys Ile Gly Ile Glu Gly Thr Met Asn Glu Asp Leu Phe Glu Asp Phe 825 830 835 840 | 2548 |
| ttg gtt aaa gaa aag caa agg gag ctt gag aaa ctt gcc atg gaa gaa Leu Val Lys Glu Lys Gln Arg Glu Leu Glu Lys Leu Ala Met Glu Glu 845 850 855 | 2596 |
| gct gaa agg agg aca cag act gaa gaa cag cgg cga aga aag gaa gca Ala Glu Arg Arg Thr Gln Thr Glu Glu Gln Arg Arg Arg Lys Glu Ala 860 865 870 | 2644 |
| agg gct gca gat gaa gct gtc agg gca caa gcg aag gcc gag ata gag Arg Ala Ala Asp Glu Ala Val Arg Ala Gln Ala Lys Ala Glu Ile Glu 875 880 885 | 2692 |
| atc aag aag aaa aaa ttg caa agt atg ttg agt ttg gcc aga aca tgt Ile Lys Lys Lys Lys Leu Gln Ser Met Leu Ser Leu Ala Arg Thr Cys 890 895 900 | 2740 |
| gtt gat aat ttg tgg tac ata gag gct agc aca gat aca aga gga gat Val Asp Asn Leu Trp Tyr Ile Glu Ala Ser Thr Asp Thr Arg Gly Asp 905 910 915 920 | 2788 |

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|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| act | atc | agg | tta | tat | tat | aac | aga | aac | tcg | agg | cca | ctt | gcg | cat | agt | 2836 |
| Thr | Ile | Arg | Leu | Tyr | Tyr | Asn | Arg | Asn | Ser | Arg | Pro | Leu | Ala | His | Ser | |
| | | | 925 | | | | | | 930 | | | | | 935 | | |
| act | gag | att | tgg | atg | cat | ggg | ggg | tac | aac | aat | tgg | aca | gat | gga | ctc | 2884 |
| Thr | Glu | Ile | Trp | Met | His | Gly | Gly | Tyr | Asn | Asn | Trp | Thr | Asp | Gly | Leu | |
| | | | 940 | | | | | 945 | | | | | 950 | | | |
| tct | att | gtt | gaa | agc | ttt | gtc | aag | tgc | aat | gac | aaa | gac | ggc | gat | tgg | 2932 |
| Ser | Ile | Val | Glu | Ser | Phe | Val | Lys | Cys | Asn | Asp | Lys | Asp | Gly | Asp | Trp | |
| | | 955 | | | | | 960 | | | | | 965 | | | | |
| tgg | tat | gca | gat | gtt | att | cca | cct | gaa | aag | gca | ctt | gtg | ttg | gac | tgg | 2980 |
| Trp | Tyr | Ala | Asp | Val | Ile | Pro | Pro | Glu | Lys | Ala | Leu | Val | Leu | Asp | Trp | |
| | 970 | | | | | 975 | | | | | 980 | | | | | |
| gtt | ttt | gct | gat | ggg | cca | gct | ggg | aat | gca | agg | aac | tat | gac | aac | aat | 3028 |
| Val | Phe | Ala | Asp | Gly | Pro | Ala | Gly | Asn | Ala | Arg | Asn | Tyr | Asp | Asn | Asn | |
| 985 | | | | | 990 | | | | | 995 | | | | | 1000 | |
| gct | cga | caa | gat | ttc | cat | gct | att | ctt | ccg | aac | aac | aat | gta | acc | gag | 3076 |
| Ala | Arg | Gln | Asp | Phe | His | Ala | Ile | Leu | Pro | Asn | Asn | Asn | Val | Thr | Glu | |
| | | | 1005 | | | | | 1010 | | | | | 1015 | | | |
| gaa | ggc | ttc | tgg | gcg | caa | gag | gag | caa | aac | atc | tat | aca | agg | ctt | ctg | 3124 |
| Glu | Gly | Phe | Trp | Ala | Gln | Glu | Glu | Gln | Asn | Ile | Tyr | Thr | Arg | Leu | Leu | |
| | | 1020 | | | | 1025 | | | | | | 1030 | | | | |
| caa | gaa | agg | aga | gaa | aag | gaa | gaa | acc | atg | aaa | aga | aag | gct | gag | aga | 3172 |
| Gln | Glu | Arg | Arg | Glu | Lys | Glu | Glu | Thr | Met | Lys | Arg | Lys | Ala | Glu | Arg | |
| | 1035 | | | | | 1040 | | | | | 1045 | | | | | |
| agt | gca | aat | atc | aaa | gct | gag | atg | aag | gca | aaa | act | atg | cga | agg | ttt | 3220 |
| Ser | Ala | Asn | Ile | Lys | Ala | Glu | Met | Lys | Ala | Lys | Thr | Met | Arg | Arg | Phe | |
| | 1050 | | | | 1055 | | | | | 1060 | | | | | | |
| ctg | ctt | tcc | cag | aaa | cac | att | gtt | tat | acc | gaa | ccg | ctt | gaa | ata | cgt | 3268 |
| Leu | Leu | Ser | Gln | Lys | His | Ile | Val | Tyr | Thr | Glu | Pro | Leu | Glu | Ile | Arg | |
| 1065 | | | | 1070 | | | | | 1075 | | | | | 1080 | | |
| gcc | gga | acc | aca | gtg | gat | gtg | cta | tac | aat | ccc | tct | aac | aca | gtg | cta | 3316 |
| Ala | Gly | Thr | Thr | Val | Asp | Val | Leu | Tyr | Asn | Pro | Ser | Asn | Thr | Val | Leu | |
| | | | 1085 | | | | | 1090 | | | | | 1095 | | | |
| aat | gga | aag | tcg | gag | ggg | tgg | ttt | aga | tgc | tcc | ttt | aac | ctt | tgg | atg | 3364 |
| Asn | Gly | Lys | Ser | Glu | Gly | Trp | Phe | Arg | Cys | Ser | Phe | Asn | Leu | Trp | Met | |
| | | 1100 | | | | | 1105 | | | | | 1110 | | | | |
| cat | tca | agt | ggg | gca | ttg | cca | ccc | cag | aag | atg | gtg | aaa | tca | ggg | gat | 3412 |
| His | Ser | Ser | Gly | Ala | Leu | Pro | Pro | Gln | Lys | Met | Val | Lys | Ser | Gly | Asp | |
| | | 1115 | | | | 1120 | | | | | 1125 | | | | | |
| ggg | ccg | ctc | tta | aaa | gca | | | | | | | | | | | |

[illegible]

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tgg tcg tgg aac cgg ccc gca ctg gac tac att gaa ttg tac cat gcc 4900
 Trp Ser Trp Asn Arg Pro Ala Leu Asp Tyr Ile Glu Leu Tyr His Ala
 1610 1615 1620

gct cga aaa ttc tgacacccaa ctgaaccaat gacaagaaca agcgcattgt 4952
Ala Arg Lys Phe
1625

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<210> 8

<211> 1628

<212> PRT

<213> Triticum aestivum

<400> 8

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Gln Pro Leu Val Val Val Arg Pro Ala Gly Arg Gly Gly Leu Thr Gln
20 25 30

Pro Phe Leu Met Asn Gly Arg Phe Thr Arg Ser Arg Thr Leu Arg Cys
35 40 45

Met Val Ala Ser Ser Asp Pro Pro Asn Arg Lys Ser Arg Arg Met Val
50 55 60

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Gln | Val | Lys | Val | Ile | Ser | Ser | Arg | Gly | Tyr | Thr | Thr | Arg | Leu |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |

Ile Val Glu Pro Ser Asn Glu Asn Thr Glu His Asn Asn Arg Asp Glu
85 90 95

Glu Thr Leu Asp Thr Tyr Asn Ala Leu Leu Ser Thr Glu Thr Ala Glu
100 105 110

Trp Thr Asp Asn Arg Glu Ala Glu Thr Ala Lys Ala Asp Ser Ser Gln
115 120 125

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ala | Leu | Ser | Ser | Ser | Ile | Ile | Gly | Glu | Val | Asp | Val | Ala | Asp | Glu |
| 130 | | | | | | 135 | | | | | | 140 | | | |
| Asp | Ile | Leu | Ala | Ala | Asp | Leu | Thr | Val | Tyr | Ser | Leu | Ser | Ser | Val | Met |
| 145 | | | | | | 150 | | | | | | 155 | | | |
| Lys | Lys | Glu | Val | Asp | Ala | Ala | Asp | Lys | Ala | Arg | Val | Lys | Glu | Asp | Ala |
| | | | 165 | | | | | | 170 | | | 175 | | | |
| Phe | Glu | Leu | Asp | Leu | Pro | Ala | Thr | Thr | Leu | Arg | Ser | Val | Ile | Val | Asp |
| | | | 180 | | | | | | 185 | | | 190 | | | |
| Val | Met | Asp | His | Asn | Gly | Thr | Val | Gln | Glu | Thr | Leu | Arg | Ser | Val | Ile |
| | | | 195 | | | | | | 200 | | | 205 | | | |
| Val | Asp | Val | Met | Asp | His | Asn | Gly | Thr | Val | Gln | Glu | Thr | Leu | Arg | Ser |
| 210 | | | | | | 215 | | | | | | 220 | | | |
| Val | Ile | Val | Asp | Val | Met | Asp | Asp | Ala | Ala | Asp | Lys | Ala | Arg | Val | Glu |
| 225 | | | | | | 230 | | | | | | 235 | | | |
| Glu | Asp | Val | Phe | Glu | Leu | Asp | Leu | Ser | Gly | Asn | Ile | Ser | Ser | Ser | Ala |
| | | | 245 | | | | | | 250 | | | 255 | | | |
| Thr | Thr | Val | Glu | Leu | Asp | Ala | Val | Asp | Glu | Val | Gly | Pro | Val | Gln | Asp |
| | | | 260 | | | | | | 265 | | | 270 | | | |
| Lys | Phe | Glu | Ala | Thr | Ser | Ser | Gly | Asn | Val | Ser | Asn | Ser | Ala | Thr | Val |
| 275 | | | | | | 280 | | | | | | 285 | | | |
| Arg | Glu | Val | Asp | Ala | Ser | Asp | Glu | Ala | Gly | Asn | Asp | Gln | Gly | Ile | Phe |
| 290 | | | | | | 295 | | | | | | 300 | | | |
| Arg | Ala | Asp | Leu | Ser | Gly | Asn | Val | Phe | Ser | Ser | Ser | Thr | Thr | Val | Glu |
| 305 | | | | | | 310 | | | | | | 315 | | | |
| Val | Gly | Ala | Val | Asp | Glu | Ala | Gly | Ser | Ile | Lys | Asp | Arg | Phe | Glu | Thr |
| | | | 325 | | | | | | 330 | | | 335 | | | |
| Asp | Ser | Ser | Gly | Asn | Val | Ser | Thr | Ser | Ala | Pro | Met | Trp | Asp | Ala | Ile |
| | | | 340 | | | | | | 345 | | | 350 | | | |
| Asp | Glu | Thr | Val | Ala | Asp | Gln | Asp | Thr | Phe | Glu | Ala | Asp | Leu | Ser | Gly |
| 355 | | | | | | 360 | | | | | | 365 | | | |
| Asn | Ala | Ser | Ser | Cys | Ala | Thr | Tyr | Arg | Glu | Val | Asp | Asp | Val | Val | Asp |
| 370 | | | | | | 375 | | | | | | 380 | | | |
| Glu | Thr | Arg | Ser | Glu | Glu | Glu | Thr | Phe | Ala | Met | Asp | Leu | Phe | Ala | Ser |
| 385 | | | | | | 390 | | | | | | 395 | | | |
| Glu | Ser | Gly | His | Glu | Lys | His | Met | Ala | Val | Asp | Tyr | Val | Gly | Glu | Ala |
| | | | 405 | | | | | | 410 | | | 415 | | | |

$$x_{j+1} = \begin{pmatrix} x_j \\ y_j \end{pmatrix}, \quad y_j = \begin{pmatrix} y_1^j \\ y_2^j \end{pmatrix}, \quad z_j = \begin{pmatrix} z_1^j \\ z_2^j \end{pmatrix}, \quad w_j = \begin{pmatrix} w_1^j \\ w_2^j \end{pmatrix}, \quad v_j = \begin{pmatrix} v_1^j \\ v_2^j \end{pmatrix}, \quad u_j = \begin{pmatrix} u_1^j \\ u_2^j \end{pmatrix},$$

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| hr | Asp | Glu | Glu | Thr | Tyr | Gln | Gln | Tyr | Pro | Val | Pro | Ser | Ser | | | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | | |
| Phe | Ser | Met | Trp | Asp | Lys | Ala | Ile | Ala | Lys | Thr | Gly | Val | Ser | Leu | Asn | | |
| | | 435 | | | | | 440 | | | | | 445 | | | | | |
| Pro | Glu | Leu | Arg | Leu | Val | Arg | Val | Glu | Glu | Gln | Gly | Lys | Val | Asn | Phe | | |
| | | 450 | | | | 455 | | | | | 460 | | | | | | |
| Ser | Asp | Lys | Lys | Asp | Leu | Ser | Ile | Asp | Asp | Leu | Pro | Gly | Gln | Asn | Gln | | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | | |
| Ser | Ile | Ile | Gly | Ser | Tyr | Lys | Gln | Asp | Lys | Ser | Ile | Ala | Asp | Val | Ala | | |
| | | | | 485 | | | | | 490 | | | | | 495 | | | |
| Gly | Pro | Thr | Gln | Ser | Ile | Phe | Gly | Ser | Ser | Lys | Gln | His | Arg | Ser | Ile | | |
| | | | 500 | | | | | 505 | | | | | 510 | | | | |
| Val | Ala | Phe | Pro | Lys | Gln | Asn | Gln | Ser | Ile | Val | Ser | Val | Thr | Glu | Gln | | |
| | | 515 | | | | | 520 | | | | | 525 | | | | | |
| Lys | Gln | Ser | Ile | Val | Gly | Phe | Arg | Ser | Gln | Asp | Leu | Ser | Ala | Val | Ser | | |
| | | 530 | | | | 535 | | | | | 540 | | | | | | |
| Leu | Pro | Lys | Gln | Asn | Val | Pro | Ile | Val | Gly | Thr | Ser | Arg | Glu | Gly | Gln | | |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 | | |
| Thr | Lys | Gln | Val | Pro | Val | Val | Asp | Arg | Gln | Asp | Ala | Leu | Tyr | Val | Asn | | |
| | | | | 565 | | | | | 570 | | | | | 575 | | | |
| Gly | Leu | Glu | Ala | Lys | Glu | Gly | Asp | His | Thr | Ser | Glu | Lys | Thr | Asp | Glu | | |
| | | | 580 | | | | | 585 | | | | | 590 | | | | |
| Asp | Ala | Leu | His | Val | Lys | Phe | Asn | Val | Asp | Asn | Val | Leu | Arg | Lys | His | | |
| | | 595 | | | | | 600 | | | | | 605 | | | | | |
| Gln | Ala | Asp | Arg | Thr | Gln | Ala | Val | Glu | Lys | Lys | Thr | Trp | Lys | Lys | Val | | |
| | | | | | | 615 | | | | | 620 | | | | | | |
| Asp | Glu | Glu | His | Leu | Tyr | Met | Thr | Glu | His | Gln | Lys | Arg | Ala | Ala | Glu | | |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 | | |
| Gly | Gln | Met | Val | Val | Asn | Glu | Asp | Glu | Leu | Ser | Ile | Thr | Glu | Ile | Gly | | |
| | | | | 645 | | | | | 650 | | | | | 655 | | | |
| Met | Gly | Arg | Gly | Asp | Lys | Ile | Gln | His | Val | Leu | Ser | Glu | Glu | Glu | Leu | | |
| | | | 660 | | | | | 665 | | | | | 670 | | | | |
| Ser | Trp | Ser | Glu | Asp | Glu | Val | Gln | Leu | Ile | Glu | Asp | Asp | Gly | Gln | Tyr | | |
| | | 675 | | | | | 680 | | | | | 685 | | | | | |
| Glu | Val | Asp | Glu | Thr | Ser | Val | Ser | Val | Asn | Val | Glu | Gln | Asp | Ile | Gln | | |
| | | | | | | 695 | | | | 700 | | | | | | | |

Asn Ala Arg Asn Tyr Asp Asn Asn Ala Arg Gln Asp Phe His Ala Ile
995 1000 1005

Leu Pro Asn Asn Asn Val Thr Glu Glu Gly Phe Trp Ala Gln Glu Glu
1010 1015 1020

Gln Asn Ile Tyr Thr Arg Leu Leu Gln Glu Arg Arg Glu Lys Glu Glu
1025 1030 1035 1040

Thr Met Lys Arg Lys Ala Glu Arg Ser Ala Asn Ile Lys Ala Glu Met
1045 1050 1055

Lys Ala Lys Thr Met Arg Arg Phe Leu Leu Ser Gln Lys His Ile Val
1060 1065 1070

Tyr Thr Glu Pro Leu Glu Ile Arg Ala Gly Thr Thr Val Asp Val Leu
1075 1080 1085

Tyr Asn Pro Ser Asn Thr Val Leu Asn Gly Lys Ser Glu Gly Trp Phe
1090 1095 1100

Arg Cys Ser Phe Asn Leu Trp Met His Ser Ser Gly Ala Leu Pro Pro
1105 1110 1115 1120

Gln Lys Met Val Lys Ser Gly Asp Gly Pro Leu Leu Lys Ala Thr Val
1125 1130 1135

Asp Val Pro Pro Asp Ala Tyr Met Met Asp Phe Val Phe Ser Glu Trp
1140 1145 1150

Glu Glu Asp Gly Ile Tyr Asp Asn Arg Asn Gly Met Asp Tyr His Ile
1155 1160 1165

Pro Val Ser Asp Ser Ile Glu Thr Glu Asn Tyr Met Arg Ile Ile His
1170 1175 1180

Ile Ala Val Glu Met Ala Pro Val Ala Lys Val Gly Gly Leu Gly Asp
1185 1190 1195 1200

Val Val Thr Ser Leu Ser Arg Ala Ile Gln Asp Leu Gly His Thr Val
1205 1210 1215

Glu Val Ile Leu Pro Lys Tyr Asp Cys Leu Asn Gln Ser Ser Val Lys
1220 1225 1230

Asp Leu His Leu Tyr Gln Ser Phe Ser Trp Gly Gly Thr Glu Ile Lys
1235 1240 1245

Val Trp Val Gly Arg Val Glu Asp Leu Thr Val Tyr Phe Leu Glu Pro
1250 1255 1260

Gln Asn Gly Met Phe Gly Val Gly Cys Val Tyr Gly Arg Asn Asp Asp
1265 1270 1275 1280

| | | | |
|---|------|------|------|
| Arg Arg Phe Gly Phe Phe Cys His Ser Ala Leu Glu Phe Ile Leu Gln | 1285 | 1290 | 1295 |
| Asn Glu Phe Ser Pro His Ile Ile His Cys His Asp Trp Ser Ser Ala | 1300 | 1305 | 1310 |
| Pro Val Ala Trp Leu Tyr Lys Glu His Tyr Ser Gln Ser Arg Met Ala | 1315 | 1320 | 1325 |
| Ser Thr Arg Val Val Phe Thr Ile His Asn Leu Glu Phe Gly Ala His | 1330 | 1335 | 1340 |
| Tyr Ile Gly Lys Ala Met Thr Tyr Cys Asp Lys Ala Thr Thr Val Ser | 1345 | 1350 | 1355 |
| Pro Thr Tyr Ser Arg Asp Val Ala Gly His Gly Ala Ile Ala Pro His | 1365 | 1370 | 1375 |
| Arg Glu Lys Phe Tyr Gly Ile Leu Asn Gly Ile Asp Pro Asp Ile Trp | 1380 | 1385 | 1390 |
| Asp Pro Tyr Thr Asp Asn Phe Ile Pro Val Pro Tyr Thr Cys Glu Asn | 1395 | 1400 | 1405 |
| Val Val Glu Gly Lys Arg Ala Ala Lys Arg Ala Leu Gln Gln Lys Phe | 1410 | 1415 | 1420 |
| Gly Leu Gln Gln Thr Asp Val Pro Ile Val Gly Ile Ile Thr Arg Leu | 1425 | 1430 | 1435 |
| Thr Ala Gln Lys Gly Ile His Leu Ile Lys His Ala Ile His Arg Thr | 1445 | 1450 | 1455 |
| Leu Glu Ser Asn Gly His Val Val Leu Leu Gly Ser Ala Pro Asp His | 1460 | 1465 | 1470 |
| Arg Ile Gln Gly Asp Phe Cys Arg Leu Ala Asp Ala Leu His Gly Val | 1475 | 1480 | 1485 |
| Tyr His Gly Arg Val Lys Leu Val Leu Thr Tyr Asp Glu Pro Leu Ser | 1490 | 1495 | 1500 |
| His Leu Ile Tyr Ala Gly Ser Asp Phe Ile Ile Val Pro Ser Ile Phe | 1505 | 1510 | 1515 |
| Glu Pro Cys Gly Leu Thr Gln Leu Val Ala Met Arg Tyr Gly Ser Ile | 1525 | 1530 | 1535 |
| Pro Ile Val Arg Lys Thr Gly Gly Leu His Asp Thr Val Phe Asp Val | 1540 | 1545 | 1550 |
| Asp Asn Asp Lys Asp Arg Ala Arg Ser Leu Gly Leu Glu Pro Asn Gly | 1555 | 1560 | 1565 |

Phe Ser Phe Asp Gly Ala Asp Ser Asn Gly Val Asp Tyr Ala Leu Asn
1570 1575 1580

Arg Ala Ile Gly Ala Trp Phe Asp Ala Arg Asp Trp Phe His Ser Leu
1585 1590 1595 1600

Cys Lys Arg Val Met Glu Gln Asp Trp Ser Trp Asn Arg Pro Ala Leu
1605 1610 1615

Asp Tyr Ile Glu Leu Tyr His Ala Ala Arg Lys Phe
1620 1625

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<213> Triticum aestivum
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<223> n can be a or g or c or t, and the encoded amino
acid cannot be assigned with certainty.
```

```
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```

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 gtggaaaaaa aaaaaaaaaa a 3621

<210> 10
 <211> 1059
 <212> PRT
 <213> Triticum aestivum

<220>
 <221> UNSURE
 <222> (1) .. (1059)
 <223> Xaa is an amino acid which could not be identified
 with certainty.

<400> 10
 Asp Ala Leu Tyr Val Asn Gly Leu Glu Ala Lys Glu Gly Asp His Thr
 1 5 10 15

London, England, 1890

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Glu | Lys | Thr | Asp | Glu | Asp | Ala | Leu | His | Val | Lys | Phe | Asn | Val | Asp | |
| | | | 20 | | | | 25 | | | | | | 30 | | | |
| Asn | Val | Leu | Arg | Lys | His | Gln | Ala | Asp | Arg | Thr | Gln | Ala | Val | Glu | Lys | |
| | | | 35 | | | | 40 | | | | | | 45 | | | |
| Lys | Thr | Trp | Lys | Lys | Val | Asp | Glu | Glu | His | Leu | Tyr | Met | Thr | Glu | His | |
| | | | 50 | | | | 55 | | | | | | 60 | | | |
| Gln | Lys | Arg | Ala | Ala | Glu | Gly | Gln | Met | Val | Val | Asn | Glu | Asp | Glu | Leu | |
| | | | 65 | | | | 70 | | | | | | 75 | 80 | | |
| Ser | Ile | Thr | Glu | Ile | Gly | Met | Gly | Arg | Gly | Asp | Lys | Ile | Gln | His | Val | |
| | | | 85 | | | | | | 90 | | | | | | 95 | |
| Leu | Ser | Glu | Glu | Glu | Leu | Ser | Trp | Ser | Glu | Asp | Glu | Val | Gln | Leu | Ile | |
| | | | 100 | | | | | | 105 | | | | | | 110 | |
| Glu | Asp | Asp | Gly | Gln | Tyr | Glu | Val | Asp | Glu | Thr | Ser | Val | Ser | Val | Asn | |
| | | | 115 | | | | | | 120 | | | | | | 125 | |
| Val | Glu | Gln | Asp | Ile | Gln | Gly | Ser | Pro | Gln | Asp | Val | Val | Asp | Pro | Gln | |
| | | | 130 | | | | | | 135 | | | | | | 140 | |
| Ala | Leu | Lys | Val | Met | Leu | Gln | Glu | Leu | Ala | Glu | Lys | Asn | Tyr | Ser | Met | |
| | | | 145 | | | | | | 150 | | | | | | 155 | 160 |
| Arg | Asn | Lys | Leu | Phe | Val | Phe | Pro | Glu | Val | Val | Lys | Ala | Asp | Ser | Val | |
| | | | 165 | | | | | | 170 | | | | | | 175 | |
| Ile | Asp | Leu | Tyr | Leu | Asn | Arg | Asp | Leu | Thr | Ala | Leu | Ala | Asn | Glu | Pro | |
| | | | 180 | | | | | | 185 | | | | | | 190 | |
| Asp | Val | Val | Ile | Lys | Gly | Ala | Phe | Asn | Gly | Trp | Lys | Trp | Arg | Leu | Phe | |
| | | | 195 | | | | | | 200 | | | | | | 205 | |
| Thr | Glu | Arg | Leu | His | Lys | Ser | Asp | Leu | Gly | Gly | Val | Trp | Trp | Ser | Cys | |
| | | | 210 | | | | | | 215 | | | | | | 220 | |
| Lys | Leu | Tyr | Ile | Pro | Lys | Glu | Ala | Tyr | Arg | Leu | Asp | Phe | Val | Phe | Phe | |
| | | | 225 | | | | | | 230 | | | | | | 235 | 240 |
| Asn | Gly | Arg | Thr | Val | Tyr | Glu | Asn | Asn | Gly | Asn | Asn | Asp | Phe | Cys | Ile | |
| | | | 245 | | | | | | 250 | | | | | | 255 | |
| Gly | Ile | Glu | Gly | Thr | Met | Asn | Glu | Asp | Leu | Phe | Glu | Asp | Phe | Leu | Val | |
| | | | 260 | | | | | | 265 | | | | | | 270 | |
| Lys | Glu | Lys | Gln | Arg | Glu | Leu | Glu | Lys | Leu | Ala | Met | Glu | Glu | Ala | Glu | |
| | | | 275 | | | | | | 280 | | | | | | 285 | |
| Arg | Arg | Thr | Gln | Thr | Glu | Glu | Gln | Arg | Arg | Arg | Lys | Glu | Ala | Arg | Ala | |
| | | | 290 | | | | | | 295 | | | | | | 300 | |

Ala Asp Glu Ala Val Arg Ala Gln Ala Lys Ala Glu Ile Glu Ile Lys
305 310 315 320

Lys Lys Lys Leu Gln Ser Met Leu Ser Leu Ala Arg Thr Cys Val Asp
325 330 335

Asn Leu Trp Tyr Ile Glu Ala Ser Thr Asp Thr Arg Gly Asp Thr Ile
340 345 350

Arg Leu Tyr Tyr Asn Arg Asn Ser Arg Pro Leu Ala His Ser Thr Glu
355 360 365

Ile Trp Met His Gly Gly Tyr Asn Asn Trp Ser Asp Gly Leu Ser Ile
370 375 380

Val Glu Ser Phe Val Lys Cys Asn Asp Lys Asp Gly Asp Trp Trp Tyr
385 390 395 400

Ala Asp Val Ile Pro Pro Glu Lys Ala Leu Val Leu Asp Trp Val Phe
405 410 415

Ala Asp Gly Pro Ala Gly Asn Ala Arg Asn Tyr Asp Asn Asn Ala Arg
420 425 430

Gln Asp Phe His Ala Ile Leu Pro Asn Asn Asn Val Thr Glu Glu Gly
435 440 445

Phe Trp Ala Gln Glu Glu Gln Asn Ile Tyr Thr Arg Leu Leu Gln Glu
450 455 460

Arg Arg Glu Lys Glu Glu Thr Met Lys Arg Lys Ala Glu Arg Ser Ala
465 470 475 480

Asn Ile Lys Ala Glu Met Lys Ala Lys Thr Met Arg Arg Phe Leu Leu
485 490 495

Ser Gln Lys His Ile Val Tyr Thr Arg Thr Xaa Leu Lys Tyr Val Pro
500 505 510

Gly Thr Thr Val Asp Val Leu Tyr Asn Pro Ser Asn Thr Val Leu Asn
515 520 525

Gly Lys Ser Glu Gly Trp Phe Arg Cys Ser Phe Asn Leu Trp Met His
530 535 540

Ser Ser Gly Ala Leu Pro Pro Gln Lys Met Val Lys Ser Gly Asp Gly
545 550 555 560

Pro Leu Leu Lys Ala Thr Val Asp Val Pro Pro Asp Ala Tyr Met Met
565 570 575

Asp Phe Val Phe Ser Glu Trp Glu Glu Asp Gly Ile Tyr Asp Asn Arg
580 585 590

cgcccgccgc ggcggcctcg cgcaggtacg ggtgattatg gttcttgatt cggtcggttc 420
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aaaaaaaaag gtttatagtg attttgattt ctttcacetc gggaacattt ttatatctgg 540
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tgagctggaa ttcatactgc ttaaaacgac gtgattttta ttgctggaag aggtaaagaa 660
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<210> 12
<211> 2446
<212> DNA
<213> Triticum sp.

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cgggaaatgc ttcaagctgc gcgacataca gagaagtgga tgatgtggtg gatgaaacta 180
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 gaatagaagg cactatgaat gaagatctgt ttgaggatgt cttggttaaa gaaaagcaaa 1560
 gggagcttga gaaacttgcc atggaagaag ctgaaaggag gacacagact gaagaacagc 1620
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 ctcgacaaga tttccatgct attcttccaa acaacaatgt aaccgaggaa ggcttctggg 2340
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<210> 13
 <211> 1032
 <212> DNA
 <213> Triticum sp.

<400> 13

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| ttttccaaat | tcaaaatgca | tggttccatg | caagcttata | caaaatcact | tgataatata | 120 |
| ccaatcacia | cataactttg | tttaccataa | gaacattcct | acttaaaatt | tgcaaggtaa | 180 |
| ctccctttcg | aggctggttg | gcttgatgag | taactggcaa | ttaacaaaga | aaagatatat | 240 |
| ctgatgtttg | gaacaaaaca | tatgatcagg | gttgtttggg | ttgactcatg | ttccttttta | 300 |
| cctacacagg | ctgagagaag | tgcaaataac | aaagctgaga | tgaaggcaaa | aactatgcga | 360 |
| aggttttctg | tttcccagaa | acacattggt | tataccgaac | cgcttgaaat | acgtgcccga | 420 |
| accacagtgg | atgtgctata | caatccctct | aacacagtgc | taaattggaaa | gccggagggt | 480 |
| tggttttagat | gctcttttaa | cctttggatg | catccaagtg | gagcattgcc | accccagaag | 540 |
| atggtgaaat | caggggatgg | gccgctctta | aaagccacag | gtttattgcg | ttattacatc | 600 |
| actgttatta | gtatatatat | aaccatthtt | atgcaatcaa | tagagtcaag | tgcaactaat | 660 |
| gatgcacaga | taggatcaca | tcattaggag | aatgatgtga | tggacaagac | ccaatcctaa | 720 |
| gcatagcaca | agatcgtgta | gttcgttcgc | tagagctttt | ctaattgtcaa | gtatcatttc | 780 |
| cttagaccat | gagattgtgc | aactcccgga | tatcgtagga | gtgctttggg | tgtatcaaat | 840 |
| gtcacaacgt | aactgggtga | ctataaagg | gcactacagg | tatctccgaa | agttttctgt | 900 |
| gggttggcac | gaatcgagac | tgggatttgt | cactccgtat | gacggagagg | tatctttggg | 960 |
| cccactcgg | aatgcatcat | cataatgagc | tcaatgtgac | taaggagtta | gccacgggat | 1020 |
| cgagaattcc | cg | | | | | 1032 |

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<210> 14
<211> 892
<212> DNA
<213> Triticum sp.
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gatatgcaac tactccctcc aatccatatt acttgtcgca actttggtac aacttttagta 120
caaagttata ctaaagctgt gacaagtaat atggaccgga gggagtacta tataagcttg 180
tagctgtttt gagaccgagt gtctgctcgg gtggctagct ggagcgggct gaagtgcttg 240
caggcacctc ttctctaaaa aaaagtgctt gcagcccccc cgccccctcc atagggtgag 300
tggtcacctt tcttcttaaa aattatggca ccaagggaaa ttctcggctg gtcgagcttg 360
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<210> 16
 <211> 1592
 <212> DNA
 <213> *Triticum* sp.

<400> 16
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 ttaccgagtg ggcccaaaga tacctctccg tcatacggag tgacaaatcc cagtctcgat 120
 tcgtgccaac ccaacagaaa ctttcggaga tacctgtagt gcacctttat agtcaccag 180
 ttacgttggtg acatttgata cacccaaagc actcctacga tatccgggag ttgcacaatc 240
 tcatggtcta aggaaatgat acttgacatt agaaaagctc tagcgaacga actacacgat 300
 cttgtgctat gcttaggatt gggctctgtc catcacatca ttctcctaata gatgtgatcc 360
 atacactgac aatttttatcc cggtagcaga ttttttccca gaggcgaagt agatatatac 420
 caaggccaca gatagtttta tgcttaacta tgtgtttcat actacttcag gtcccttata 480
 cttgtgagaa tgttgctgaa ggcaagagag ctgcaaaaag ggccttgagc cagaagtttg 540
 gattacagca aactgatgtc cctattgtcg gaatcatcac ccgtctgaca gccagaagg 600
 gaatccacct catcaagcac gcaattcacc gaaccctcga aagcaacgga cagggttcac 660
 atcccttggtg aacgaataaa catcaaacgt tttgtttata aaaagttgct tactatttgt 720
 ttttgtttac ttcaaaacaa aagtctgaaa atgaagtgtt tgggttcctag gtgggtttgc 780
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 tggtagagctc caatatccta cacaccatct agccagccct tcattatggg agctggagac 960
 tactttataa ttttaggttga tgatcgatca tgctgcagat atacgctggc tccgacttca 1020
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 gatcgatccc tatagttcgg aaaaccggag gtgtgtgact atttctctcc attatgctgc 1140
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 gactttacga cactgtcttc gacgtagaca atgataagga ccgggctcgg tctcttggtc 1260
 ttgaacaaaa tgggttcagt ttcgacggag ccgacagcaa cggcgtggat tatgcctca 1320
 acaggcaagt atcgttcctc aattagccct gaattcagca gtagtgctag gttatttacc 1380
 ttgcatgttc catacctcat ttcagagcaa tcggcgcttg gttcgatgcc cgtgattggg 1440
 tccactccct gtgtaagagg gtcattggaac aagactgggc atggaaccgg cccgcactgg 1500

[illegible]

actacattga attgtaccat gccgctcgaa aattctgaca cccaactgaa ccaatggcaa 1560

gaacaagcgc attgtgggat cgagaattcc cg 1592

<210> 17

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:peptide motif

<400> 17

Asp Val Gln Leu Val Met Leu Gly Thr Gly

| | | |
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| 1 | 5 | 10 |
|---|---|----|

<210> 18

<211> 10

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence:peptide motif

<400> 18

Ala Ala Gly Lys Lys Asp Ala Gly Ile Asp

1 5 10

<210> 19

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:peptide motif

<400> 19

Ala Thr Gly Lys Lys Asp Ala Gly Ile Asp

1 5 10

<210> 20

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:peptide motif

<400> 20

Ala Leu Gly Lys Lys Asp Ala Gly Ile Asp

1 5 10

<210> 21
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:peptide motif

<400> 21
 Ala Thr Gly Lys Lys Asp Ala Leu
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<210> 22
 <211> 8
 <212> PRT
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<220>
 <223> Description of Artificial Sequence:peptide motif

<400> 22
 Ala Leu Gly Lys Lys Asp Ala Leu
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<210> 23
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:peptide motif

<400> 23
 Ala Ala Gly Lys Lys Asp Ala Arg Val Asp Asp Asp Ala Ala
 1 5 10

<210> 24
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:peptide motif

<400> 24
 Ala Leu Gly Lys Lys Asp Ala Gly Ile Val Asp Gly Ala
 1 5 10

<210> 25
 <211> 23

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 useful as a primer

<400> 25
 tgttgaggtt ccatggcacg ttc 23

<210> 26
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 useful as a primer

<400> 26
 agtcgttctg ccgtatgatg tcg 23

<210> 27
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
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 useful as a primer

<400> 27
 ccaagtacca gtggtgaacg c 21

<210> 28
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 useful as a primer

<400> 28
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<210> 29
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
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 useful as a primer

<400> 29
 ggaggtcttg gtgatgttgt 20

<210> 30
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 useful as a primer

<400> 30
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<210> 31
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 useful as a primer

<400> 31
 cattgccatg attggtcaag 20

<210> 32
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 useful as a primer

<400> 32
 accacctgtc cgttccgttg c 21

<210> 33
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 useful as a primer

<400> 33
gcacggtcta tgagaacaat ggc 23

<210> 34
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
useful as a primer

<400> 34
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<210> 35
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide motif

<400> 35
Lys Val Gly Gly Leu Gly Asp Val Val Thr Ser Leu Ser Arg Ala Val
1 5 10 15

<210> 36
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide motif

<400> 36
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1 5 10 15

Gln Asp Leu Gly His Asn Val Glu Val
20 25

<210> 37
<211> 9024
<212> DNA
<213> Triticum sp.

<400> 37
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taatggataa aaaataaaac atcaaagaaa aacgaaatgc agaagaaaaa aacgtcactt 120

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|------|
| gttcccttat | tatctcccggt | gcaccccggt | agcgtaggac | aaaaagaaaa | aatagaacggt | 180 |
| acccaacgtc | acaagctcac | acatgcccag | cgagagaaaa | gaaaaatggt | gcgacaaaaa | 240 |
| aaaggaaacg | ggctgagagc | cgaaacacat | gggctgcgct | ttgttcgcta | cgaagctctc | 300 |
| ccctcgacaa | aatatgaatc | gcgacgtgat | tggatcctat | ggtggaaaaa | gtgaatgaga | 360 |
| ccaaaagaat | tctcagctga | atgagtttta | gcaagactga | tcattatatc | caacataaat | 420 |
| agattttttt | tttgcaaaaa | taatccaaat | ctattagcaa | agttcagtag | aagtacaaag | 480 |
| catctcgaac | attataaaca | ttacactgag | attccaggac | caccaaaca | cccactactg | 540 |
| ccgcgaaaag | aaaaggattc | ggaagacaga | aattatccaa | accacgttcg | tccttggttg | 600 |
| ttggtctcat | tgcgcgctaa | acaacctgga | cagcagaaga | agcaaagcag | tgtgcttccg | 660 |
| ctccgcagca | agaagacaag | tcgtcacatg | tcagacgccg | tactcaagc | aagcaaactg | 720 |
| caatgcttct | cgttcggttt | atcccctagc | acgcacgaac | gcatgtgccg | caccgcgtca | 780 |
| cgcaacgcat | gcatgcacaa | accaacaaac | gaaacagtgc | agttgcagtg | ctctatctac | 840 |
| atatacgcaa | tcaacgcggg | cctcctcctt | cgccgcgagc | cccgttccgt | cctcggtctt | 900 |
| cacgtggatt | ttgcaacttc | cttcacgcag | cttgtcacca | cggacgcttc | ctctctgaca | 960 |
| actggccccg | tgggcggaac | ggggcctccg | ctcgcccctt | gcgaaaccca | cggtcgcgtc | 1020 |
| gttcgcttct | ctagcgggca | ccgacagaag | gggcgcggcg | agggtaggac | caggctgtca | 1080 |
| gctggtgagg | agcctgccgc | tcgttggtgc | gcagctggag | accgagcggg | gcaacggaac | 1140 |
| ggctgccgcc | ctcgtgtgct | gctcgcgtgg | cacgcgcgca | cggcacccgg | cccgccttcc | 1200 |
| agcgtgctcg | cccgcaaacc | gcagacccaa | cacgccagcc | gccagggggc | cgttcgtacg | 1260 |
| taccgcgcc | tcgtgtaaag | ccgcgcgcgt | cgtcgcgcgc | ccccgctcgc | ggccatttct | 1320 |
| tcggcctgac | cccgttcgtt | tacccccaca | cagagcacac | tccagtccag | tccagcccac | 1380 |
| tgccaccgcg | ctactctcca | ctcccactgc | caccacctcc | gcctgcgcgc | cgtctctgggc | 1440 |
| ggaccaaccc | gcgaaccgta | ccatctcccg | ccccgatcca | tgctcgtcgg | ggtcgcgtcc | 1500 |
| gccgcacct | tcctcgcgct | cgcgtcagcc | tccccgggga | gatcacgcag | gcgggcgagg | 1560 |
| gtgagcgcgc | agccacccca | cgccggggcc | ggcaggttgc | actggccgcc | gtggccgcgc | 1620 |
| cagcgcacgg | ctcgcgacgg | agctgtggcg | gcgctcgcgc | ccgggaagaa | ggacgcgggg | 1680 |
| atcgacgacg | ccgccgcgtc | cgtgaggcag | ccccgcgcac | tccgcggtgg | cgccgccacc | 1740 |
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cgctcacgaa ttgtttatatt atacaaaacg cagccccgcg tgtgcaggtc ggggagcgaa 1860
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10015418-057902
Rec'd PCT/PTO 07 MAY 2002

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of:

Morell et al.

: Group Art Unit: Not yet assigned

Serial No: 10/018,418

: Examiner: Not yet assigned

371 Filing date: October 29, 2001 : Confirmation No. 1169

Int. Filing Date: April 28, 2000

For: GENES ENCODING WHEAT STARCH
SYNTHASES AND USES THEREFOR
(as amended)

| CERTIFICATE OF MAILING | |
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SECOND PRELIMINARY AMENDMENT

Commissioner for Patents
Washington, D.C. 20231

Sir:

Please enter the following amendments:

In the Specification:

At page 1, after the title, please insert:

CROSS REFERENCE TO RELATED APPLICATIONS

This application was filed under 35 U.S.C. 371, based on PCT/AU00/00385, which application was filed April 28, 2000 and claims priority from Australian Patent Application No. PQ0052/99 filed April 29, 1999.

REMARKS

Applicants have amended the application to include a paragraph providing cross reference to related applications

It is believed that this amendment does not necessitate the payment of any fees under 37 C.F.R. 1.16-1.17. If this is incorrect, however, please charge any fee due under the foregoing Rules to Deposit Account No. 07-1969.

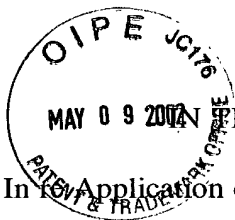
Respectfully submitted,



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Attorney docket No. 127-01
bmk: May 7, 2002



10038418-050902
Rec'd PCT/PTO 09 MAY 2002

THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

Morell et al. : Group Art Unit: Not yet assigned

Serial No: 10/018,418 : Examiner: Not yet assigned

371 Filing date: October 29, 2001 : Confirmation No. 1169

Int. Filing Date: April 28, 2000

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SYNTHASES AND USES THEREFOR
(as amended)

CERTIFICATE OF MAILING

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Date

B. Kroge
B. Kroge

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Attorney docket No. 127-01
bmk: May 9, 2002

10/018418

- 1 -

NOVEL GENES ENCODING WHEAT STARCH SYNTHASES
AND USES THEREFOR

FIELD OF THE INVENTION

5 The present invention relates generally to isolated nucleic acid molecules encoding wheat starch synthase enzymes and more particularly, to isolated nucleic acid molecules that encode wheat SSII and SSIII enzyme activities. The isolated nucleic acid molecules provide the means for modifying starch content and composition in plants, for example the ratio of amylose:amylopectin in the starch granule of the
10 endosperm during the grain-filling phase of endosperm development. The isolated nucleic acid molecules of the present invention also provide the means for screening plant lines to determine the presence of natural and/or induced mutations in starch synthase genes which affect starch content and/or composition. The isolated nucleic acid molecules of the present invention further provide for the screening-assisted
15 breeding of plants having desirable starch content and/or composition, in addition to providing for the direct genetic manipulation of plant starch content and/or composition.

GENERAL

Bibliographic details of the publications numerically referred to in this specification are
20 collected at the end of the description. Reference herein to any published document is not to be taken as an indication or admission that any such published document is part of the common general knowledge or background information of a skilled worker in the relevant field.

25 This specification contains nucleotide and amino acid sequence information (SEQ ID NOS:) prepared using the programme PatentIn Version 2.0, presented herein at the end of the specification. Each nucleotide or amino acid sequence is identified in the sequence listing by the numeric indicator <210> followed by the sequence identifier (e.g. <210>1, <210>2, etc). The length, type of sequence (DNA, protein (PRT), etc)
30 and source organism for each nucleotide or amino acid sequence are indicated by information provided in the numeric indicator fields <211>, <212> and <213>.

- 2 -

respectively. Nucleotide and amino acid sequences (SEQ ID NOs:) referred to in the specification are defined by the information provided in numeric indicator field <400> followed by the sequence identifier (eg. SEQ ID NO: 1 is <400>1, etc).

- 5 The designation of nucleotide residues referred to herein are those recommended by the IUPAC-IUB Biochemical Nomenclature Commission, wherein A represents Adenine, C represents Cytosine, G represents Guanine, T represents thymine, Y represents a pyrimidine residue, R represents a purine residue, M represents Adenine or Cytosine, K represents Guanine or Thymine, S represents Guanine or Cytosine, W
10 represents Adenine or Thymine, H represents a nucleotide other than Guanine, B represents a nucleotide other than Adenine, V represents a nucleotide other than Thymine, D represents a nucleotide other than Cytosine and N represents any nucleotide residue.
- 15 The designations for naturally-occurring amino acid residues referred to herein are set forth in Table I. The designations for a non-limiting set of non-naturally-occurring amino acids is listed in Table 2.

As used herein the term "derived from" shall be taken to indicate that a specified
20 integer may be obtained from a particular source albeit not necessarily directly from that source.

Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to
25 imply the inclusion of a stated step or element or integer or group of steps or elements or integers but not the exclusion of any other step or element or integer or group of steps or elements or integers.

- 3 -

TABLE 1

| Amino Acid | Three-letter Code | One-letter Code |
|-------------------------|-------------------|-----------------|
| 5 Alanine | Ala | A |
| Arginine | Arg | R |
| Asparagine | Asn | N |
| Aspartic acid | Asp | D |
| Cysteine | Cys | C |
| 10 Glutamine | Gln | Q |
| Glutamic acid | Glu | E |
| Glycine | Gly | G |
| Histidine | His | H |
| Isoleucine | Ile | I |
| 15 Leucine | Leu | L |
| Lysine | Lys | K |
| Methionine | Met | M |
| Phenylalanine | Phe | F |
| Proline | Pro | P |
| 20 Serine | Ser | S |
| Threonine | Thr | T |
| Tryptophan | Trp | W |
| Tyrosine | Tyr | Y |
| Valine | Val | V |
| 25 Aspartate/glutamate | Baa | B |
| Asparagine/glutamine | | |
| Any amino acid as above | Xaa | X |

TABLE 2

| Non-conventional amino acid | Code | Non-conventional amino acid | Code |
|---|-------|--------------------------------|--------|
| 5 α -aminobutyric acid | Abu | L-N-methylalanine | Nmala |
| α -amino- α -methylbutyrate | Mgabu | L-N-methylarginine | Nmarg |
| aminocyclopropane- carboxylate | Cpro | L-N-methylasparagine | Nmasn |
| 10 aminoisobutyric acid | Aib | L-N-methylaspartic acid | Nmasp |
| aminonorbornyl- carboxylate | Norb | L-N-methylcysteine | Nmcys |
| cyclohexylalanine | Chexa | L-N-methylglutamine | Nmgln |
| cyclopentylalanine | Cpen | L-N-methylglutamic acid | Nmglu |
| 15 D-alanine | Dal | L-N-methylhistidine | Nmhis |
| D-arginine | Darg | L-N-methylisoleucine | Nmile |
| D-aspartic acid | Dasp | L-N-methylleucine | Nmleu |
| D-cysteine | Dcys | L-N-methyllysine | Nmlys |
| D-glutamine | Dgln | L-N-methylmethionine | Nmmet |
| 20 D-glutamic acid | Dglu | L-N-methylnorleucine | Nmnle |
| D-histidine | Dhis | L-N-methylnorvaline | Nmnva |
| D-isoleucine | Dile | L-N-methylornithine | Nmorn |
| D-leucine | Dleu | L-N-methylphenylalanine | Nmphe |
| D-lysine | Dlys | L-N-methylproline | Nmpro |
| 25 D-methionine | Dmet | L-N-methylserine | Nmser |
| D-ornithine | Dorn | L-N-methylthreonine | Nmthr |
| D-phenylalanine | Dphe | L-N-methyltryptophan | Nmtrp |
| D-proline | Dpro | L-N-methyltyrosine | Nmtyr |
| D-serine | Dser | L-N-methylvaline | Nmval |
| 30 D-threonine | Dthr | L-N-methylethylglycine | Nmetg |
| D-tryptophan | Dtrp | L-N-methyl-t-butylglycine | Nmtbug |
| | | L-norleucine | Nle |
| | | L-norvaline | Nva |

- 5 -

| | | | | |
|----|----------------------------------|--------|---|--------|
| | D-tyrosine | Dtyr | α -methyl-aminoisobutyrate | Maib |
| | D-valine | Dval | α -methyl- γ -aminobutyrate | Mgabv |
| | D- α -methylalanine | Dmala | α -methylcyclohexylalanine | Mchexa |
| | D- α -methylarginine | Dmarg | α -methylcyclopentylalanine | Mcpen |
| 5 | D- α -methylasparagine | Dmasn | α -methyl- α -naphthylalanine | Manap |
| | D- α -methylaspartate | Dmasp | α -methylpenicillamine | Mpen |
| | D- α -methylcysteine | Dmcys | N-(4-aminobutyl)glycine | Nglu |
| | D- α -methylglutamine | Dmgln | N-(2-aminoethyl)glycine | Naeg |
| | D- α -methylhistidine | Dmhis | N-(3-aminopropyl)glycine | Norn |
| 10 | D- α -methylisoleucine | Dmile | N-amino- α -methylbutyrate | Nmaabu |
| | D- α -methylleucine | Dmleu | α -naphthylalanine | Anap |
| | D- α -methyllysine | Dmlys | N-benzylglycine | Nphe |
| | D- α -methylmethionine | Dmmet | N-(2-carbamylethyl)glycine | Ngln |
| | D- α -methylornithine | Dmorn | N-(carbamylmethyl)glycine | Nasn |
| 15 | D- α -methylphenylalanine | Dmphe | N-(2-carboxyethyl)glycine | Nglu |
| | D- α -methylproline | Dmpro | N-(carboxymethyl)glycine | Nasp |
| | D- α -methylserine | Dmser | N-cyclobutylglycine | Ncbut |
| | D- α -methylthreonine | Dmthr | N-cycloheptylglycine | Nchep |
| | D- α -methyltryptophan | Dmtrp | N-cyclohexylglycine | Nchex |
| 20 | D- α -methyltyrosine | Dmtty | N-cyclodecylglycine | Ncdec |
| | D- α -methylvaline | Dmval | N-cylcododecylglycine | Ncdod |
| | D-N-methylalanine | Dnmala | N-cyclooctylglycine | Ncoct |
| | D-N-methylarginine | Dnmarg | N-cyclopropylglycine | Ncpro |
| | D-N-methylasparagine | Dnmasn | N-cycloundecylglycine | Ncund |
| 25 | D-N-methylaspartate | Dnmasp | N-(2,2-diphenylethyl) glycine | Nbhm |
| | D-N-methylcysteine | Dnmcys | N-(3,3-diphenylpropyl) glycine | Nbhe |

- 6 -

| | | | | |
|----|-------------------------------|---------|---|--------|
| | D-N-methylglutamine | Dnmglu | N-(3-guanidinopropyl) glycine | Narg |
| | D-N-methylglutamate | Dnmglu | N-(1-hydroxyethyl)glycine | Nthr |
| | D-N-methylhistidine | Dnmhis | N-(hydroxyethyl)glycine | Nser |
| 5 | D-N-methylisoleucine | Dnmile | N-(imidazolylethyl) glycine | Nhis |
| | D-N-methylleucine | Dnmleu | N-(3-indolylethyl) glycine | Nhtrp |
| | D-N-methyllysine | Dnmlys | N-methyl- γ -aminobutyrate | Nmgabu |
| 10 | N-methylcyclohexylalanine | Nmchexa | D-N-methylmethionine | Dnmmt |
| | D-N-methylornithine | Dnmorn | N-methylcyclopentylalanine | Nmcpn |
| | N-methylglycine | Nala | D-N-methylphenylalanine | Dnmphe |
| | N-methylaminoisobutyrate | Nmaib | D-N-methylproline | Dnmpro |
| | N-(1-methylpropyl)glycine | Nile | D-N-methylserine | Dnmser |
| 15 | N-(2-methylpropyl)glycine | Nleu | D-N-methylthreonine | Dnmthr |
| | D-N-methyltryptophan | Dnmtrp | N-(1-methylethyl)glycine | Nval |
| | D-N-methyltyrosine | Dnmtyr | N-methyl- α -naphthylalanine | Nmanap |
| | D-N-methylvaline | Dnmval | N-methylpenicillamine | Nmpen |
| | γ -aminobutyric acid | Gabu | N-(<i>p</i> -hydroxyphenyl)glycine | Nhtyr |
| 20 | L- <i>t</i> -butylglycine | Tbug | N-(thiomethyl)glycine | Ncys |
| | L-ethylglycine | Etg | penicillamine | Pen |
| | L-homophenylalanine | Hphe | L- α -methylalanine | Mala |
| | L- α -methylarginine | Marg | L- α -methylasparagine | Masn |
| | L- α -methylaspartate | Masp | L- α -methyl- <i>t</i> -butylglycine | Mtbug |
| 25 | L- α -methylcysteine | Mcys | L-methylethylglycine | Metg |
| | L- α -methylglutamine | Mglu | L- α -methylglutamate | Mglu |
| | L- α -methylhistidine | Mhis | L- α -methylhomo phenylalanine | Mhphe |
| | L- α -methylisoleucine | Mile | N-(2-methylthioethyl) glycine | Nmet |
| 30 | L- α -methylleucine | Mleu | L- α -methyllysine | Mlys |

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| | | | |
|----------------------------------|-------|-------------------------------|-------|
| L- α -methylmethionine | Mmet | L- α -methylnorleucine | Mnle |
| L- α -methylnorvaline | Mnva | L- α -methylornithine | Morn |
| L- α -methylphenylalanine | Mphe | L- α -methylproline | Mpro |
| L- α -methylserine | Mser | L- α -methylthreonine | Mthr |
| 5 L- α -methyltryptophan | Mtrp | L- α -methyltyrosine | Mtyr |
| L- α -methylvaline | Mval | L-N-methylhomo | |
| | | phenylalanine | Nmhpe |
| N-(N-(2,2-diphenylethyl) | | N-(N-(3,3-diphenylpropyl) | |
| carbanylmethyl)glycine | Nnbhm | carbanylmethyl)glycine | Nnbhe |
| 10 1-carboxy-1-(2,2-diphenyl- | | | |
| ethylamino)cyclopropane | Nmbc | | |

Those skilled in the art will appreciate that the invention described herein is susceptible
 15 to variations and modifications other than those specifically described. It is to be
 understood that the invention includes all such variations and modifications. The
 invention also includes all of the steps, features, compositions and compounds
 referred to or indicated in this specification, individually or collectively, and any and all
 combinations or any two or more of said steps or features.

20

The present invention is not to be limited in scope by the specific embodiments
 described herein, which are intended for the purposes of exemplification only.
 Functionally-equivalent products, compositions and methods are clearly within the
 scope of the invention, as described herein.

25

BACKGROUND TO THE INVENTION

The biosynthesis of the starch granule is a complex process which involves the action
 of an array of isoforms of enzymes involved in the starch biosynthesis. Following the
 formation of glucose-1-phosphate, the enzyme activities required for the synthesis of
 30 granular starch include ADP glucose pyrophosphorylase (EC 2.7.7.27), starch
 synthases (EC 2.4.1.21), branching enzymes (EC 2.4.1.18) and debranching enzymes

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(EC 3.2.1.41 and EC 3.2.1.68) (Mouille *et al.*, 1996). Plants contain isozymes of each of these activities, and the definition of these isoforms and their roles has been conducted through investigation of the properties of the suite of soluble enzymes found in the stroma of the plastid, analysis of the proteins entrapped within the matrix of the starch granule, and mutational studies to identify genes and define linkages between individual genes and their specific roles.

Starch synthases extend regions of α -1,4 glucan through the transfer of the glucosyl moiety of ADPglucose to the non-reducing end of a pre-existing α -1,4 glucan. In addition to GBSS, 3 other classes of starch synthase have been identified in plants, SSI (wheat, Li *et al.*, 1999 and GenBank Accession No. U48227; rice, Baba *et al.*, 1993; potato, Genbank Accession No. STSTASYNT), SSII (pea, Dry *et al.* 1992; potato, Edwards *et al.*, 1995; maize, Harn *et al.* 1998 and GenBank Accession No. U66377) and SSIII (potato, Abel *et al.*, 1996; maize, Gao *et al.*, 1998). In the cereals, the most comprehensively studied species is maize, where in addition to GBSS, cDNAs encoding SSI, SSIIa, and SSIIb have been isolated, and both cDNA and genomic clones for *dull1* have been characterised (Knight *et al.*, 1998; Harn *et al.*, 1998; Gao *et al.*, 1998). In maize, the product of the *du1* gene is known as maize SSII, however this gene is the homologue of potato SSIII.

20

The proteins within the matrix of the wheat starch granule have been extensively studied (Denyer *et al.*, 1995; Rahman *et al.*, 1995; Takaoka *et al.*, 1997; Yamamori and Endo, 1996) and 60, 75, 85, 100, 104 and 105 kDa protein bands can be visualised following SDS-PAGE. The predominant 60 kDa protein is exclusively granule-bound and is analogous to the "waxy" granule bound starch synthase (GBSS) gene in maize (Rahman *et al.*, 1995). The combination of three null alleles for this enzyme from each of the wheat genomes (Nakamura *et al.*, 1995) results in the amylose-free "waxy" phenotype found in other species. The 75 kDa starch synthase I (wSSI) is found in both the granule and the soluble fraction of wheat endosperm (Denyer *et al.*, 1995; Li *et al.*, 1999) and has been assigned to chromosomes 7A, 7B and 7D (Yamamori and Endo, 1996; Li *et al.*, 1999). The 85 kDa band contains a

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class II branching enzyme and an unidentified polypeptide (Rahman *et al.*, 1995). The 100, 104 and 105 kDa proteins of the wheat starch granule (designated Sgp-B1, Sgp-D1 and Sgp-A1 by Yamamori and Endo, 1996) have been shown to be encoded by a homeologous set of genes on the short arm of chromosome 7B, 7A and 7D 5 respectively (Yamamori and Endo, 1996; Takaoka *et al.*, 1997). Denyer *et al.* (1995) concluded on the basis of enzyme activity assays that these proteins were also starch synthases. These genes are referred to hereinafter as the "wheat SSII genes".

While GBSS has been established to be essential for amylose synthesis, the remaining 10 starch synthases are thought to be primarily responsible for the elongation of amylopectin chains, although this does not preclude them from also having non-essential roles in amylose biosynthesis. Differences in kinetic properties between isoforms, and the analysis of mutants lacking various isoforms, suggests that each isoenzyme contributes to the extension of specific subsets of the available non- 15 reducing ends.

SUMMARY OF THE INVENTION

The production of plants that produce improved starches that are modified for particular end-use applications, such as, for example, starches having high or low 20 amylose:amylopectin ratios, requires the availability of genes encoding the various starch synthase isoforms. Because of species-specific codon usages, and variations in the kinetic parameters of the starch synthase isoforms between species, the production of modified starches may require the use of genes derived from particular species.

25

Furthermore, the screening-assisted breeding of plants having desirable starch content and/or composition requires specific gene sequences to be provided that can be used to distinguish between different homeologous genes encoding the various isoforms of wheat starch synthases, such as, for example, to identify and distinguish between 30 naturally-occurring variant gene sequences. It is a particular object of the present invention to provide gene sequences to facilitate the screening-assisted selection of

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wheat plants having starch traits which are associated with the presence and/or expression of one or more wheat SSI and/or SSIII genes.

Accordingly, the present invention provides isolated nucleotide sequences encoding
5 the wheat SSII (i.e. wSSII) and wheat SSIII (i.e. wSSIII) isoenzymes, and DNA markers derived therefrom. The present invention further facilitates the production of transformed plants carrying these nucleotide sequences.

More particularly, the present invention provides isolated nucleic acid molecules
10 encoding the 100, 104 and 105 kDa SSII (Sgp-1) polypeptides of the wheat starch granule matrix, as determined using the SDS/PAGE system of Rahman *et al.* (1995), which polypeptides are equivalent to the 100, 108 and 115 kDa polypeptides described by Yamamori and Endo (1996).

15 The present invention further provides isolated nucleic acid molecules encoding the soluble *dull1*-type wheat starch synthase III polypeptide. Analysis of the polypeptides encoded by these nucleic acid molecules reveals several consensus amino acid sequence motifs that are highly conserved in wheat starch synthase isoenzymes, in addition to isoenzyme-specific sequences, which sequences possess utility in isolating
20 related starch synthase-encoding sequences and in assaying plants for their expression of one or more starch synthase isoenzymes.

Accordingly, one aspect of the present invention provides an isolated nucleic acid molecule which comprises a sequence of nucleotides which encodes, or is
25 complementary to a nucleic acid molecule which encodes a wheat starch synthase polypeptide, protein or enzyme molecule or a functional subunit thereof selected from the following:

- (i) a wheat starch synthase II (wSSII) polypeptide, protein or enzyme or functional subunit thereof which comprises an amino acid sequence which is at
30 least about 85% identical overall to an amino acid sequence set forth in any one of SEQ ID NOS: 2, 4, or 6;

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(ii) a wheat starch synthase III (wSSIII) polypeptide, protein or enzyme or functional subunit thereof which comprises an amino acid sequence which is at least about 85% identical overall to an amino acid sequence set forth in any one of SEQ ID NOS: 8 or 10;

5 (iii) a wheat starch synthase polypeptide, protein or enzyme or functional subunit thereof which comprises a conserved amino acid sequence having at least 25% identity to an amino acid sequence selected from the group consisting of:

- 10 (a) KVGGLGDVVTS (SEQ ID NO: 39);
- (b) GHTVEVILPKY (SEQ ID NO: 40);
- (c) HDWSSAPVAWLYKEHY (SEQ ID NO: 41);
- (d) GILNGIDPDIWDPYTD (SEQ ID NO: 42);
- (e) DVPIVGIIITRLTAQKG (SEQ ID NO: 43);
- (f) NGQVVLLGSA (SEQ ID NO: 44);
- 15 (g) AGSDFIIVPSIFPCGLTQLVAMRYGS (SEQ ID NO: 45); and
- (h) TGGLVDTV (SEQ ID NO: 46);

wherein said wheat starch synthase polypeptide further comprises an amino acid sequence having at least about 85% identity overall to an amino acid sequence set forth in any one of SEQ ID NOS: 2, 4, 6, 8 or 10; and

20 (iv) a wheat starch synthase polypeptide, protein or enzyme or functional subunit thereof which comprises a conserved amino acid sequence having at least 25% identity to an amino acid sequence selected from the group consisting of:

- 25 (a) KTGGLGDVAGA (SEQ ID NO: 47);
- (b) GHRVMVVVPRY (SEQ ID NO: 48);
- (c) NDWHTALLPVYLKAYY (SEQ ID NO: 49);
- (d) GIVNGIDNMEWNPEVD (SEQ ID NO: 50);
- (e) DVPLLGFIGRLDGQKG (SEQ ID NO: 51);
- (f) DVQLVMLGTG (SEQ ID NO: 52);
- 30 (g) AGADALLMPSTRF(E/V)PCGLNQLYAMAYGT (SEQ ID NO: 53); and
- (h) VGG(V/L)RDTV (SEQ ID NO: 54);

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wherein said wheat starch synthase polypeptide further comprises an amino acid sequence having at least about 85% identity overall to an amino acid sequence set forth in any one of SEQ ID NOS: 2, 4, 6, 8 or 10.

5 In a preferred embodiment, the isolated nucleic acid molecule encodes a starch synthase polypeptide, protein or enzyme having at least about 90% amino acid sequence identity to any one of SEQ ID NOS: 2, 4, 6, 8 or 10, more preferably having at least about 95% or about 97% or about 99% identity to any one of said amino acid sequences.

10

In an alternative embodiment, the isolated nucleic acid molecule of the present invention encodes a wheat starch synthase polypeptide which comprises one or more amino acid sequences selected from the group consisting of:

- (a) GHTVEVILPKY;
- 15 (b) HDWSSAPVAWLYKEHY;
- (c) DVPIVGIITRLTAQKG;
- (d) NGQVVLLGSA;
- (e) AGSDFIIVPSIFPCGLTQLVAMRYGS;
- (f) TGGLVDTV;
- 20 (g) GIVNGIDNMEWNPEVD; and
- (h) AGADALLMPSTRF(E/V)PCGLNQLYAMAYGT.

in an alternative embodiment, the present invention provides an isolated nucleic acid molecule which encodes a wheat starch synthase polypeptide, protein or enzyme
25 molecule or a functional subunit thereof, wherein said nucleic acid molecule comprises a nucleotide sequence having at least about 85% nucleotide sequence identity to any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37 or 38 or a complementary nucleotide sequence thereto.

30 In a preferred embodiment, the isolated nucleic acid molecule comprises the nucleotide sequence set forth in any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37 or 38,

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or is at least about 90% identical, more preferably at least about 95% or 97% or 99% identical to all or a protein-encoding part thereof.

In an alternative embodiment, the present invention provides an isolated nucleic acid
5 molecule which encodes a wheat starch synthase polypeptide, protein or enzyme molecule or a functional subunit thereof, wherein said nucleic acid molecule comprises a nucleotide sequence that is capable of hybridising under at least moderate stringency hybridisation conditions to at least about 30 contiguous nucleotides derived from any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37 or 38, or a complementary
10 nucleotide sequence thereto.

A second aspect of the present invention provides a method of isolating a nucleic acid molecule that encodes a starch synthase polypeptide, protein or enzyme described *supra*, said method comprising:

- 15 (i) hybridising a probe or primer comprising at least about 15 contiguous nucleotides in length derived from any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37 or 38, or a complementary nucleotide sequence thereto to single-stranded or double-stranded mRNA, cDNA or genomic DNA; and
(ii) detecting the hybridised mRNA, cDNA or genomic DNA using a detecting
20 means.

Preferably, the detecting means is a reporter molecule covalently attached to the probe or primer molecule or alternatively, a polymerase chain reaction format. Accordingly, the present invention clearly extends to the use of the nucleic acid molecules provided
25 herein to isolate related starch synthase-encoding sequences using standard hybridisation and/or polymerase chain reaction techniques.

A third aspect of the invention provides an isolated probe or primer comprising at least about 15 contiguous nucleotides in length derived from any one of SEQ ID NOS: 1, 3,
30 5, 7, 9, 11-16, 37 or 38, or a complementary nucleotide sequence thereto.

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Preferably, the probe or primer comprises a nucleotide sequence set forth in any one of SEQ ID NOS: 25 to 34.

A fourth aspect of the present invention is directed to an isolated or recombinant starch
5 synthase polypeptide, protein or enzyme, preferably substantially free of conspecific or non-specific proteins, which comprises an amino acid sequence selected from the following:

- 10 (i) a wheat starch synthase II (wSSII) polypeptide, protein or enzyme or functional subunit thereof which comprises an amino acid sequence which is at least about 85% identical overall to an amino acid sequence set forth in any one of SEQ ID NOS: 2, 4, or 6;
- (ii) a wheat starch synthase III (wSSIII) polypeptide, protein or enzyme or functional subunit thereof which comprises an amino acid sequence which is at
15 least about 85% identical overall to an amino acid sequence set forth in any one of SEQ ID NOS: 8 or 10;
- (iii) a wheat starch synthase polypeptide, protein or enzyme or functional subunit thereof which comprises a conserved amino acid sequence having at least 25% identity to an amino acid sequence selected from the group consisting of:
 - 20 (a) KVGGLGDVVTs;
 - (b) GHTVEVILPKY;
 - (c) HDWSSAPVAWLYKEHY;
 - (d) GILNGIDPDIWDPYTD;
 - (e) DVPIVGIIITRLTAQKG;
 - 25 (f) NGQVVLLGSA;
 - (g) AGSDFIIVPSIFPCGLTQLVAMRYGS; and
 - (h) TGGLVDTV

wherein said wheat starch synthase polypeptide further comprises an amino acid sequence having at least about 85% identity overall to an amino acid
30 sequence set forth in any one of SEQ ID NOS: 2, 4, 6, 8 or 10; and

- (iv) a wheat starch synthase polypeptide, protein or enzyme or functional

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subunit thereof which comprises a conserved amino acid sequence having at least 25% identity to an amino acid sequence selected from the group consisting of:

- (a) KTGGLGDVAGA;
- 5 (b) GHRVMVVVPRY;
- (c) NDWHTALLPVYLKAYY;
- (d) GIVNGIDNMEWNPEVD;
- (e) DVPLLGFGRDLGQKG;
- (f) DVQLVMLGTG;
- 10 (g) AGADALLMPSRF(E/V)PCGLNQLYAMAYGT; and
- (h) VGG(V/L)RDTV

wherein said wheat starch synthase polypeptide further comprises an amino acid sequence having at least about 85% identity overall to an amino acid sequence set forth in any one of SEQ ID NOS: 2, 4, 6, 8 or 10.

15

The present invention clearly encompasses the mature protein region of a wheat starch synthase polypeptide which is obtained by removal of the N-terminal transit peptide sequence.

- 20 A further aspect of the invention provides a method of assaying for the presence or absence of a starch synthase isoenzyme or the copy number of a gene encoding same in a plant, comprising contacting a biological sample derived from said plant with an isolated nucleic acid molecule derived from any one of SEQ ID NOS 1, 3, 5, 7, 9, 11-16, 37 or 38, or any one of SEQ ID NOS: 25 to 34, or a complementary nucleotide
- 25 sequence thereto for a time and under conditions sufficient for hybridisation to occur and then detecting said hybridisation using a detection means.

The detection means according to this aspect of the invention is any nucleic acid based hybridisation or amplification reaction.

30

A further aspect of the present invention utilises the above-mentioned assay method

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in the breeding and/or selection of plants which express or do not express particular starch synthase isoenzymes or alternatively, which express a particular starch synthase isoenzyme at a particular level in one or more plant tissues. This aspect clearly extends to the selection of transformed plant material which contains one or
5 more of the isolated nucleic acid molecules of the present invention.

A further aspect of the present invention provides a method of modifying the starch content and/or starch composition of one or more tissues or organs of a plant, comprising expressing therein a sense molecule, antisense molecule, ribozyme
10 molecule, co-suppression molecule, or gene-targeting molecule having at least about 85% nucleotide sequence identity to any one of any one of SEQ ID NOS: 1, 3, 5, 7, 9,11-16, 37 or 38, or a complementary nucleotide sequence thereto for a time and under conditions sufficient for the enzyme activity of one or more starch synthase isoenzymes to be modified. This aspect of the invention clearly extends to the
15 introduction of the sense molecule, antisense molecule, ribozyme molecule, co-suppression molecule, or gene-targeting molecule to isolated plant cells, tissues or organs or organelles by cell fusion or transgenic means and the regeneration of intact plants therefrom.

20 A further aspect of the present invention provides an isolated promoter that is operable in the endosperm of a monocotyledonous plant cell, tissue or organ, and preferably in the endosperm of a monocotyledonous plant cell, tissue or organ. For example, the HMG promoter from wheat, or the maize zein gene promoter are particularly preferred, as is the promoter derived from a starch synthase gene of the present invention, such
25 as a promoter that is linked *in vivo* to any one of SEQ ID NOS 1, 3, 5, 7, 9,11-16, 37 or 38, or a complementary nucleotide sequence thereto.

A still further aspect of the present invention contemplates a transgenic plant comprising an introduced sense molecule, antisense molecule, ribozyme molecule, co-
30 suppression molecule, or gene-targeting molecule having at least about 85% nucleotide sequence identity to any one of any one of SEQ ID NOS: 1, 3, 5, 7, 9,11-16,

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37 or 38, or a complementary nucleotide sequence thereto or a genetic construct comprising same, and to plant propagules, cells, tissues, organs or plant parts derived from said transgenic plant that also carry the introduced molecule(s).

5 BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a copy of a photographic representation showing the distribution of wheat endosperm starch synthases between the starch granule and soluble fractions. Lane 1, SDS-PAGE of wheat endosperm starch granule proteins revealed by silver staining; lanes 2-7, immunoblot of wheat endosperm soluble phase and starch granule proteins separated by SDS-PAGE from various developmental stages and probed with an anti- (wheat wSSII peptide) monoclonal antibody. Lanes 2-4 contain proteins from the soluble fraction of wheat endosperm at 15 days post anthesis (Lane 2); 20 days post anthesis (Lane 3); and at 25 days post anthesis (Lane 4). Lanes 5-7 contain proteins from the starch granule of wheat endosperm at 15 days post anthesis (Lane 5); 20 days post anthesis (Lane 6); and at 25 days post anthesis (Lane 7).

Figure 2 is a copy of a schematic representation comparing the nucleotide sequences of cDNA clones designated wSSIIA, wSSIIB and wSSIID, encoding the starch synthase II polypeptides from wheat, using the PILEUP programme of Devereaux *et al.* (1984).

Figure 3 is a copy of a schematic representation comparing the deduced amino acid sequences of starch synthase II from wheat (wSSIIA, wSSIIB and wSSIID), maize (maize SSIIa and maize SSIIb; Harn *et al.*, 1998), pea (pea SSII; Dry *et al.*, 1992) and potato (potato SSII; van der Leij *et al.*, 1991). Identical amino acid residues among each of these sequences are indicated below the sequences with "*". The alignments of maize SSIIa with maize SSIIb, and pea SSII and potato SSII are essentially as described in Harn *et al.* (1998) and Edwards *et al.* (1995). All sequences are aligned to position the transit peptide cleavage site below the arrow (↓) between residues 59 and 60 of the wSSIIA sequence. The wSSIIp1 sequence, the sequence of SGP-B1 (peptide3), and of eight conserved regions are annotated and underlined.

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Figure 4 is a copy of a photographic representation of a northern blot showing the expression of wheat wSSII mRNA in wheat plants. Total RNAs were isolated from leaves pre-anthesis florets and endosperm of the wheat cultivar "Gabo", grown under a photoperiod comprising 16 hours daylength, and at 18 °C during the day, and at 13 °C during the night cycle, and probed with the wSSIIp2 DNA fragment. The source of each RNA is indicated at the top of the Figure as follows: Lane 1, leaf; Lane 2, pre-anthesis florets; Lanes 3-11, endosperm at: 4 days post-anthesis (Lane 3); 6 days post-anthesis (Lane 4); 8 days post-anthesis (Lane 5); 10 days post-anthesis (Lane 6); 12 days post-anthesis (Lane 7); 15 days post-anthesis (Lane 8); 18 days post-anthesis (Lane 9); 21 days post-anthesis (Lane 10); and 25 days post-anthesis (Lane 11).

Figure 5 is a copy of a photographic representation showing the localization of wheat starch synthase II genes on the wheat genome by PCR, using the primers ssIIc, ssIIId and ssIIe in the amplification reaction. The nullisomic-tetrasomic genomic DNA of wheat cv. Chinese Spring was used as template DNA. Lane D, *Triticum tauschii*; Lane AB, Accession line N7DT7B having no 7D chromosome and four copies of the 7B chromosome; Lane AD, Accession line N7BT7A having no 7B chromosome and four copies of the 7A chromosome; Lane BD, Accession line N7AT7B having no 7A chromosome and four copies of the 7B chromosome; Lane ABD, wheat cv. Chinese Spring. PCR products derived from each cDNA clone are labelled. The results indicate that the cDNA clones, wSSIIb, wSSIIa and wSSIIId are derived from the B-, A- and D-genomes of wheat, respectively.

Figure 6 is a schematic representation showing the organisation of introns (lines) and exons (boxes) in the wheat SSII gene shown in SEQ ID NO: 37. The scale (bases), relative to the nucleotide sequence set forth in SEQ ID NO: 37, is provided at the bottom of the figure.

Figure 7 is a schematic representation comparing the deduced amino acid Sequences of the maize, potato and wheat SSIII polypeptides.

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Figure 8 is a copy of a photographic representation showing the expression of wheat wSSIII mRNA in wheat. Total RNAs were isolated from the endosperm of the wheat cultivars Wyuna (Panel a) and Gabo (Panel b) leaves pre-anthesis florets and endosperm of the wheat cultivar "Gabo", grown under a photoperiod comprising 16 hours daylength, and at 18 °C during the day cycle, and at 13 °C during the night cycle, and probed with the wSSIIIp1 DNA fragment derived from wSSIII.B3 cDNA. The source of each RNA is indicated at the top of the Figure as follows: Lane 1, endosperm at: 4 days post-anthesis; Lane 2, endosperm at 6 days post-anthesis; Lane 4, endosperm at 8 days post-anthesis; Lane 4, endosperm at 10 days post-anthesis; 10 Lane 5, endosperm at 12 days post-anthesis; Lane 6, endosperm at 15 days post-anthesis; Lane 7, endosperm at 18 days post-anthesis; Lane 8, endosperm at 21 days post-anthesis; Lane 9, endosperm at 25 days post-anthesis; and Lane 10, endosperm at 31 days post-anthesis (Panel a only). In panel (c), L refers to leaf RNA, and P refers to RNA from pre-anthesis florets derived from the cultivar Gabo.

15

Figure 9 is a schematic representation showing the position of conserved amino acid sequences within four wheat starch synthase proteins. The eight highly-conserved regions between the wheat starch synthase polypeptides are underlined and annotated at the top of each group of amino acid sequences. The sequences included in the 20 alignment are the wheat SSII-A1 and wheat SSIII polypeptides of the present invention; wheat GBSS (wGBSS; Yan *et al.*, 1999); wheat SSI (wSS1; Li *et al.*, 1999); wheat SSII (wSS2; SEQ ID NO: 4); and wheat SSIII (wSS3; SEQ ID NO: 8).

Figure 10 is a schematic representation showing the relationships between the 25 primary amino acid sequences of starch synthases (SS) and glycogen synthase of *E. coli* (GS). The dendrogram was generated by the program PILEUP (Devereaux *et al.*, 1984). The amino acid sequences used for the analysis are those of the wheat SSIIA, wheat SSIIIB, wheat SSIIID, and wheat SSIII polypeptides of the present invention compared to the deduced amino acid sequences of wheat GBSS (Clark *et al.*, 1991), 30 wheat SSI (Li *et al.*, 1999), rice GBSS (Okagaki, 1992), rice SSI (Baba *et al.*, 1993), maize GBSS (Kloesgen *et al.*, 1986), maize SSI (Knight *et al.*, 1998), maize SSIIa and

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maize SSIIb (Harn *et al.*, 1998), maize SSIII (Gao *et al.*, 1998), pea GBSS (Dry *et al.*, 1992), pea SSII (Dry *et al.*, 1992), potato GBSS (van der Leij *et al.*, 1991), potato SSI (Genbank accession number: STSTASYNT), potato SSII (Edwards *et al.*, 1995), potato SSIII (Abel *et al.*, 1996), and *E. coli* glycogen synthase (GS) (Kumar *et al.*, 1986). Five groups of enzymes included in the alignment are granule-bound starch synthase (GBSS), starch synthase-I (SSI), starch synthase-II (SSII), starch synthase-III (SSIII) and glycogen synthase (GS).

Figure 11 is a schematic representation showing the position of conserved regions within cereal starch synthase genes. Comparisons of cereal starch synthases were made based on their deduced amino acid sequences and 8 conserved regions identified. Conserved regions are shown in bold and transit peptides (where defined) in grey. The sequences included in the alignment are the wheat SSII-A1 and wheat SSIII polypeptides of the present invention; wheat GBSS (Ainsworth *et al.*, 1993); wheat SSI (Li *et al.*, 1999); maize SSIIa (Harn *et al.*, 1998); and maize dull-1 (Gao *et al.*, 1998).

Figure 12 is a copy of a schematic representation of a gene map showing the alignment of fragments 1 to 6 of the genomic SSIII gene (lower line) with the corresponding SSIII cDNA clone (upper line). Raised regions in the genomic clone fragments (lower line) represent protein-encoding regions of the gene.

Figure 13 is a schematic representation showing the organisation of introns (lines) and exons (boxes) in the wheat SSIII gene shown in SEQ ID NO: 38. The scale (bases), relative to the nucleotide sequence set forth in SEQ ID NO: 38, is provided at the bottom of the figure.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

One aspect of the present invention provides an isolated nucleic acid molecule which comprises a sequence of nucleotides which encodes, or is complementary to a nucleic

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acid molecule which encodes a wheat starch synthase polypeptide, protein or enzyme molecule or a functional subunit thereof selected from the following:

- (i) a wheat starch synthase II (wSSII) polypeptide, protein or enzyme or functional subunit thereof which comprises an amino acid sequence set forth in any one of SEQ ID NOS: 2, 4, or 6; and
- (ii) a wheat starch synthase III (wSSIII) polypeptide, protein or enzyme or functional subunit thereof which comprises an amino acid sequence set forth in any one of SEQ ID NOS: 8 or 10.

10 Alternatively or in addition, the isolated nucleic acid molecule of the present invention encodes a wheat starch synthase II (wSSII) polypeptide, protein or enzyme or functional subunit thereof and comprises a nucleotide sequence set forth in any one of SEQ ID NOS: 1, 3, 5, or 37.

15 Alternatively or in addition, the isolated nucleic acid molecule of the present invention encodes a wheat starch synthase III (wSSIII) polypeptide, protein or enzyme or functional subunit thereof and comprises a nucleotide sequence set forth in any one of SEQ ID NOS: 7, 9, or 38.

20 As used herein, the term "starch synthase" shall be taken to refer to any enzymatically-active peptide, polypeptide, oligopeptide, polypeptide, protein or enzyme molecule that is at least capable of transferring a glucosyl moiety from ADP-glucose to an α -1,4-glucan molecule, or a peptide, polypeptide, oligopeptide or polypeptide fragment of such an enzymatically-active molecule.

25

The term "wheat starch synthase" refers to a starch synthase derived from hexaploid wheat or barley or a progenitor species, or a relative thereto such as the diploid *Triticum tauschii* or other diploid, tetraploid, aneuploid, polyploid, nullisomic, or a wheat/barley addition line, amongst others, the only requirement that the genomic DNA is at least about 80% identical to the genome of a wheat plant as determined by standard DNA melting curve analyses.

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The term "starch synthase II" or "wSSII" or similar term shall be taken to refer to a starch synthase as hereinbefore defined that is detectable in the starch granule of a plant seed endosperm and possesses one or more properties selected from the group consisting of:

- 5 (i) it is immunologically cross-reactive with the wheat starch granule proteins designated Sgp-B1 and/or Sgp-D1 and/or Sgp-A1, having estimated molecular weights of about 85 kDa to about 115 kDa;
- (ii) it is encoded by one of a homeologous set of genes localised on wheat chromosomes 7B or 7A or 7D;
- 10 (iii) it is encoded by a nucleotide sequence that comprises at least about 15 nucleotides in length derived from any one or more of SEQ ID NOS: 1, 3, 5, or 37 or a complementary nucleotide sequence thereto;
- (iv) it is encoded by a nucleotide sequence that is at least about 85% identical to one or more of the nucleotide sequences set forth in SEQ ID NOS:
- 15 1, 3, 5, or 37, or a complementary nucleotide sequence thereto;
- (v) it comprises an amino acid sequence having at least about 85% identity to one or more of SEQ ID NOS: 2 or 4 or 6;
- (vi) it comprises at least about 5 contiguous amino acids, preferably at least about 10 contiguous amino acids, more preferably at least about 15 contiguous amino acids, even more preferably at least about 20 contiguous amino acids
- 20 and still even more preferably at least about 25-50 contiguous amino acids of the amino acid sequences set forth in SEQ ID NOS: 2 or 4 or 6;
- (vii) it which comprises a conserved amino acid sequence having at least 25% identity to an amino acid sequence selected from the group consisting of:
- 25 (a) KVGGLGDVVTS;
- (b) GHTVEVILPKY;
- (c) HDWSSAPVAWLYKEHY;
- (d) GILNGIDPDIWDPYTD;
- (e) DVPIVGIIITRLTAQKG;
- 30 (f) NGQVVLLGSA;
- (g) AGSDFIIVPSIFPCGLTQLVAMRYGS; and

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(h)TGGLVDTV,

in addition to any one or more of (i) to (vi); and

(viii) it which comprises a conserved amino acid sequence having at least 25% identity to an amino acid sequence selected from the group consisting of:

- 5 (a) KTGGLGDVAGA;
- (b) GHRVMVVVPRY;
- (c) NDWHTALLPVYLKAYY;
- (d) GIVNGIDNMEWNPEVD;
- (e) DVPLLGFIGRLDGQKG;
- 10 (f) DVQLVMLGTG;
- (g)AGADALLMPSRF(E/V)PCGLNQLYAMAYGT; and
- (h)VGG(V/L)RDTV,

in addition to any one or more of (i) to (vi).

15 The term "starch synthase III" or "wSSIII" or similar term shall be taken to refer to a starch synthase as hereinbefore defined that possesses one or more properties selected from the group consisting of:

- (i) it is encoded by a nucleotide sequence that comprises at least about 15 nucleotides in length derived from any one or more of SEQ ID NOS: 7, 9, 11-20 16, or 38, or a complementary nucleotide sequence thereto;
- (ii) it is encoded by a nucleotide sequence that is at least about 85% identical to one or more of the nucleotide sequences set forth in SEQ ID NOS: 7, 9, 11-16, or 38, or a complementary nucleotide sequence thereto; and
- (iii) it comprises an amino acid sequence having at least about 85% identity25 to one or more of SEQ ID NOS: 8 or 10;
- (iv) it comprises at least about 5 contiguous amino acids, preferably at least about 10 contiguous amino acids, more preferably at least about 15 contiguous amino acids, even more preferably at least about 20 contiguous amino acids and still even more preferably at least about 25-50 contiguous amino acids of30 the amino acid sequences set forth in SEQ ID NOS: 8 or 10;
- (v) which comprises a conserved amino acid sequence having at least 25%

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identity to an amino acid sequence selected from the group consisting of:

- (a) KVGGLGDVVTS;
- (b) GHTVEVILPKY;
- (c) HDWSSAPVAWLYKEHY;
- (d) GILNGIDPDIWDPYTD;
- (e) DVPIVGIIITRLTAQKG;
- (f) NGQVVLLGSA;
- (g) AGSDFIIVPSIFEPCGLTQLVAMRYGS; and
- (h) TGGLVDTV

in addition to any one or more of (i) to (iv); and

(vi) it which comprises a conserved amino acid sequence having at least 25% identity to an amino acid sequence selected from the group consisting of:

- (a) KTGGLGDVAGA;
- (b) GHRVMVVVPRY;
- (c) NDWHTALLPVYLKAYY;
- (d) GIVNGIDNMEWNPEVD;
- (e) DVPLLGFIRLDGQKG;
- (f) DVQLVMLGTG;
- (g) AGADALLMPSRF(E/V)PCGLNQLYAMAYGT; and
- (h) VGG(V/L)RDTV,

in addition to any one or more of (i) to (iv).

In a more preferred embodiment, the WSSII or WSSIII polypeptide encoded by the nucleic acid molecule of the present invention will comprise a substantial contiguous region of any one of SEQ ID NOS: 2, 4, 6, 8 or 10 or 17 sufficient to possess the biological activity of a starch synthase polypeptide.

For the purposes of nomenclature, the nucleotide sequence set forth in SEQ ID NO: 1 relates to the cDNA molecule encoding the WSSII (i.e. Sgp-B1) polypeptide of wheat. The amino acid sequence of the corresponding polypeptide is set forth herein as SEQ ID NO:2. The nucleotide sequence set forth in SEQ ID NO: 3 relates to the

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cDNA molecule encoding the WSSII (i.e. Sgp-A1) polypeptide of wheat. The amino acid sequence of the corresponding polypeptide is set forth herein as SEQ ID NO:4. The nucleotide sequence set forth in SEQ ID NO: 5 relates to the cDNA molecule encoding the WSSII (i.e. Sgp-D1) polypeptide of wheat. The amino acid sequence of the corresponding polypeptide is set forth herein as SEQ ID NO:6. The nucleotide sequences set forth in SEQ ID NOs: 7 and 9 relate, respectively, to full-length and partial cDNA molecules encoding the WSSIII polypeptide of wheat. The amino acid sequences of the corresponding polypeptides are set forth herein as SEQ ID NOS: 8 and 10, respectively. The nucleotide sequences set forth in SEQ ID NOs: 11 to 16 relates to fragments of the genomic gene encoding the WSSIII polypeptide of wheat, significant protein-encoding regions of which are described by reference to Table 4 and Figure 11. The nucleotide sequence set forth in SEQ ID NO: 37 relates to the WSSII genomic gene of *Triticum tauschii*, corresponding to the WSSII gene of the D-genome of wheat, which encodes the WSSIII polypeptide. The nucleotide sequence set forth in SEQ ID NO: 38 relates to the wheat WSSIII genomic gene.

Preferably, the isolated nucleic acid molecule of the present invention comprises a sequence of nucleotides which encodes, or is complementary to a nucleic acid molecule which encodes a wheat starch synthase polypeptide, protein or enzyme molecule or a functional subunit thereof which comprises an amino acid sequence which is at least about 85% identical overall to an amino acid sequence set forth in any one of SEQ ID NOS: 2, 4, 6, 8, or 10 and more preferably, which additionally comprises which comprises one or more amino acid sequences selected from the group consisting of:

- 25 (a) KVGGLGDVVTS;
(b) GHTVEVILPKY;
(c) HDWSSAPVAWLYKEHY;
(d) GILNGIDPDIWDPYTD;
(e) DVPIVGIIITRLTAQKG;
30 (f) NGQVVLLGSA;
(g) AGSDFIIVPSIFEPGLTQLVAMRYGS;

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- (h)TGGLVDTV;
- (i) KTGGLGDVAGA;
- (j) GHRVMVVVPRY;
- (k) NDWHTALLPVYLKAYY;
- 5 (l) GIVNGIDNMEWNPEVD;
- (m) DVPLLGFIGRLDGQKG;
- (n) DVQLVMLGTG;
- (o)AGADALLMPSRF(E/V)PCGLNQLYAMAYGT; and
- (p)VGG(V/L)RDTV.

10

The present invention clearly extends to homologues, analogues and derivatives of the wheat starch synthase II and III genes exemplified by the nucleotide sequences set forth herein as SEQ ID NOs: 1, 3, 5, 7, 9, 11-16, 37 or 38.

15 Preferred starch synthase genes may be derived from a naturally-occurring starch synthase gene by standard recombinant techniques. Generally, a starch synthase gene may be subjected to mutagenesis to produce single or multiple nucleotide substitutions, deletions and/or additions. Nucleotide insertional derivatives of the starch synthase gene of the present invention include 5' and 3' terminal fusions as
20 well as intra-sequence insertions of single or multiple nucleotides. Insertional nucleotide sequence variants are those in which one or more nucleotides are introduced into a predetermined site in the nucleotide sequence although random insertion is also possible with suitable screening of the resulting product. Deletional variants are characterised by the removal of one or more nucleotides from the
25 sequence. Substitutional nucleotide variants are those in which at least one nucleotide in the sequence has been removed and a different nucleotide inserted in its place. Such a substitution may be "silent" in that the substitution does not change the amino acid defined by the codon. Alternatively, substituents are designed to alter one amino acid for another similar acting amino acid, or amino acid of like charge, polarity, or
30 hydrophobicity.

For the present purpose, "homologues" of a nucleotide sequence shall be taken to

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refer to an isolated nucleic acid molecule which is substantially the same as the nucleic acid molecule of the present invention or its complementary nucleotide sequence, notwithstanding the occurrence within said sequence, of one or more nucleotide substitutions, insertions, deletions, or rearrangements.

5

"Analogues" of a nucleotide sequence set forth herein shall be taken to refer to an isolated nucleic acid molecule which is substantially the same as a nucleic acid molecule of the present invention or its complementary nucleotide sequence, notwithstanding the occurrence of any non-nucleotide constituents not normally
10 present in said isolated nucleic acid molecule, for example carbohydrates, radiochemicals including radionucleotides, reporter molecules such as, but not limited to DIG, alkaline phosphatase or horseradish peroxidase, amongst others.

"Derivatives" of a nucleotide sequence set forth herein shall be taken to refer to any
15 isolated nucleic acid molecule which contains significant sequence similarity to said sequence or a part thereof. Generally, the nucleotide sequence of the present invention may be subjected to mutagenesis to produce single or multiple nucleotide substitutions, deletions and/or insertions. Nucleotide insertional derivatives of the nucleotide sequence of the present invention include 5' and 3' terminal fusions as well
20 as intra-sequence insertions of single or multiple nucleotides or nucleotide analogues. Insertional nucleotide sequence variants are those in which one or more nucleotides or nucleotide analogues are introduced into a predetermined site in the nucleotide sequence of said sequence, although random insertion is also possible with suitable screening of the resulting product being performed. Deletional variants are
25 characterised by the removal of one or more nucleotides from the nucleotide sequence. Substitutional nucleotide variants are those in which at least one nucleotide in the sequence has been removed and a different nucleotide or nucleotide analogue inserted in its place.

30 The present invention extends to the isolated nucleic acid molecule when integrated into the genome of a cell as an addition to the endogenous cellular complement of starch synthase genes, irrespective of whether or not the introduced nucleotide

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sequence is translatable or non-translatable to produce a polypeptide. The present invention clearly contemplates the introduction of additional copies of starch synthase genes into plants, particularly wheat plants, in the antisense orientation to reduce the expression of particular wheat starch synthase genes. As will be known to those skilled in the art, such antisense genes are non-translatable, notwithstanding that they can be expressed to produce antisense mRNA molecules.

The said integrated nucleic acid molecule may, or may not, contain promoter sequences to regulate expression of the subject genetic sequence.

10

Accordingly, the present invention clearly encompasses preferred homologues, analogues and derivatives that comprise a sequence of nucleotides which encodes, or is complementary to a nucleic acid molecule which encodes a wheat starch synthase polypeptide, protein or enzyme molecule or a functional subunit thereof

15 selected from the following:

- (i) a wheat starch synthase II (wSSII) polypeptide, protein or enzyme or functional subunit thereof which comprises an amino acid sequence which is at least about 85% identical overall to an amino acid sequence set forth in any one of SEQ ID NOS: 2, 4, or 6;
- 20 (ii) a wheat starch synthase III (wSSIII) polypeptide, protein or enzyme or functional subunit thereof which comprises an amino acid sequence which is at least about 85% identical overall to an amino acid sequence set forth in any one of SEQ ID NOS: 8 or 10;
- (iii) a wheat starch synthase polypeptide, protein or enzyme or functional subunit thereof which comprises a conserved amino acid sequence having at least 25% identity to an amino acid sequence selected from the group consisting of:
 - (a) KVGGLGDVVT;
 - (b) GHTVEVILPKY;
 - 30 (c) HDWSSAPVAWLYKEHY;
 - (d) GILNGIDPDIWDPYTD;

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(e) DVPIVGIIITRLTAQKG;

(f) NGQVVLLGSA;

(g)AGSDFIIVPSIFEPGLTQLVAMRYGS; and

(h)TGGLVDTV

5 and wherein said wheat starch synthase polypeptide further comprises an amino acid sequence having at least about 85% identity overall to an amino acid sequence set forth in any one of SEQ ID NOS: 2, 4, 6, 8 or 10; and
(iv) a wheat starch synthase polypeptide, protein or enzyme or functional subunit thereof which comprises a conserved amino acid sequence having at
10 least 25% identity to an amino acid sequence selected from the group consisting of:

(a) KTGGLGDVAGA;

(b) GHRVMVVVPRY;

(c) NDWHTALLPVYLKAYY;

15 (d) GIVNGIDNMEWNPEVD;

(e) DVPLLGFGRDLGQKG;

(f) DVQLVMLGTG;

(g)AGADALLMPSRF(E/V)PCGLNQLYAMAYGT; and

(h)VGG(V/L)RDTV,

20 and wherein said wheat starch synthase polypeptide further comprises an amino acid sequence having at least about 85% identity overall to an amino acid sequence set forth in any one of SEQ ID NOS: 2, 4, 6, 8 or 10.

Preferably, the isolated nucleic acid molecule encodes a starch synthase polypeptide,
25 protein or enzyme that comprises two, more preferably three, more preferably four, more preferably five, more preferably six, more preferably seven and even more preferably eight of the conserved amino acid motifs listed *supra*. Even more preferably, the said amino acid motifs are located in a relative configuration such as that shown for the wheat SSII or wheat SSIII polypeptides described herein.

30

In a preferred embodiment, the isolated nucleic acid molecule encodes a starch

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synthase polypeptide, protein or enzyme having at least about 90% amino acid sequence identity to any one of SEQ ID NOS: 2, 4, 6, 8 or 10, more preferably having at least about 95% or about 97% or about 99% identity to any one of said amino acid sequences.

5

In an alternative embodiment, the present invention provides an isolated nucleic acid molecule which encodes a wheat starch synthase polypeptide, protein or enzyme molecule or a functional subunit thereof, wherein said nucleic acid molecule comprises a nucleotide sequence having at least about 85% nucleotide sequence identity to any
10 one of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37, or 38, or a degenerate nucleotide sequence thereto or a complementary nucleotide sequence thereto.

By "degenerate nucleotide sequence" is meant a nucleotide sequence that encodes a substantially identical amino acid sequence as a stated nucleotide sequence.

15

In a preferred embodiment, the isolated nucleic acid molecule comprises the nucleotide sequence set forth in any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37, or 38, or is at least about 90% identical, more preferably at least about 95% or 97% or 99% identical to all or a protein-encoding part thereof.

20

In an alternative embodiment, preferred homologues, analogues and derivatives of the nucleic acid molecule of the present invention encodes a wheat starch synthase polypeptide, protein or enzyme molecule or a functional subunit thereof and comprises a nucleotide sequence that is capable of hybridising under at least moderate
25 stringency hybridisation conditions to at least about 30 contiguous nucleotides derived from any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37, or 38, or a complementary nucleotide sequence thereto.

For the purposes of defining the level of stringency, a low stringency is defined herein
30 as being a hybridisation and/or a wash carried out in 6xSSC buffer, 0.1% (w/v) SDS at 28°C. Generally, the stringency is increased by reducing the concentration of SSC

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buffer, and/or increasing the concentration of SDS and/or increasing the temperature of the hybridisation and/or wash. A moderate stringency comprises a hybridisation and/or a wash carried out in 0.2 x SSC-2 x SSC buffer, 0.1% (w/v) SDS at 42°C to 65°C, while a high stringency comprises a hybridisation and/or a wash carried out in
5 0.1xSSC-0.2 x SSC buffer, 0.1% (w/v) SDS at a temperature of at least 55°C. Conditions for hybridisations and washes are well understood by one normally skilled in the art. For the purposes of further clarification only, reference to the parameters affecting hybridisation between nucleic acid molecules is found in pages 2.10.8 to 2.10.16. of Ausubel *et al.* (1987), which is herein incorporated by reference.

10

Those skilled in the art will be aware of procedures for the isolation of further wheat starch synthase genes to those specifically described herein or homologues, analogues or derivatives of said genes, for example further cDNA sequences and genomic gene equivalents, when provided with one or more of the nucleotide
15 sequences set forth in SEQ ID NOs: 1, 3, 5, 7, 9,11-16, 37, or 38. In particular, amplifications and/or hybridisations may be performed using one or more nucleic acid primers or hybridisation probes comprising at least 10 contiguous nucleotides and preferably at least about 20 contiguous nucleotides or 50 contiguous nucleotides derived from the nucleotide sequences set forth herein, to isolate cDNA clones, mRNA
20 molecules, genomic clones from a genomic library (in particular genomic clones containing the entire 5' upstream region of the gene including the promoter sequence, and the entire coding region and 3'-untranslated sequences), and/or synthetic oligonucleotide molecules, amongst others. The present invention clearly extends to such related sequences.

25

Accordingly, a second aspect of the present invention provides a method of isolating a nucleic acid molecule that encodes a starch synthase polypeptide, protein or enzyme said method comprising:

- 30 (i) hybridising a probe or primer comprising at least about 15 contiguous nucleotides in length derived from any one of SEQ ID NOS 1, 3, 5, 7, 9,11-16, 37, or 38, or a complementary nucleotide sequence thereto to single-stranded or double-stranded mRNA, cDNA or genomic DNA; and

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- (ii) detecting the hybridised mRNA, cDNA or genomic DNA using a detecting means.

Preferably, the detecting means is a reporter molecule covalently attached to the probe
5 or primer molecule or alternatively, a polymerase chain reaction format.

An alternative method contemplated in the present invention involves hybridising two nucleic acid "primer molecules" to a nucleic acid "template molecule" which comprises a related starch synthase gene or related starch synthase genetic sequence or a
10 functional part thereof, wherein the first of said primers comprises contiguous nucleotides derived from any one or more of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37, or 38, and the second of said primers comprises contiguous nucleotides complementary to any one or more of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37, or 38. Specific nucleic acid molecule copies of the template molecule are amplified enzymatically in a
15 polymerase chain reaction, a technique that is well known to one skilled in the art.

In a preferred embodiment, each nucleic acid primer molecule is at least 10 nucleotides in length, more preferably at least 20 nucleotides in length, even more preferably at least 30 nucleotides in length, still more preferably at least 40 nucleotides
20 in length and even still more preferably at least 50 nucleotides in length.

Furthermore, the nucleic acid primer molecules consists of a combination of any of the nucleotides adenine, cytidine, guanine, thymidine, or inosine, or functional analogues or derivatives thereof which are at least capable of being incorporated into a
25 polynucleotide molecule without having an inhibitory effect on the hybridisation of said primer to the template molecule in the environment in which it is used.

Furthermore, one or both of the nucleic acid primer molecules may be contained in an aqueous mixture of other nucleic acid primer molecules, for example a mixture of
30 degenerate primer sequences which vary from each other by one or more nucleotide substitutions or deletions. Alternatively, one or both of the nucleic acid primer molecules may be in a substantially pure form.

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The nucleic acid template molecule may be in a recombinant form, in a virus particle, bacteriophage particle, yeast cell, animal cell, or a plant cell. Preferably, the nucleic acid template molecule is derived from a plant cell, tissue or organ, in particular a cell, tissue or organ derived from a wheat or barley plant or a progenitor species, or a
5 relative thereto such as the diploid *Triticum tauschii* or other diploid, tetraploid, aneuploid, polyploid, nullisomic, or a wheat/barley addition line, amongst others.

Those skilled in the art will be aware that there are many known variations of the basic polymerase chain reaction procedure, which may be employed to isolate a related
10 starch synthase gene or related starch synthase genetic sequence when provided with the nucleotide sequences set forth herein. Such variations are discussed, for example, in McPherson *et al* (1991). The present invention extends to the use of all such variations in the isolation of related starch synthase genes or related starch synthase genetic sequences using the nucleotide sequences embodied by the present invention.
15

As exemplified herein, the present inventors have isolated several wheat starch synthase genes using both hybridisation and polymerase chain reaction approaches, employing novel probes and primer sequences to do so.

20 Accordingly, a third aspect of the invention provides an isolated probe or primer comprising at least about 15 contiguous nucleotides in length derived from any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37, or 38, or a complementary nucleotide sequence thereto.

25 Preferably, the probe or primer comprises a nucleotide sequence set forth in any one of SEQ ID NOS: 25 to 34.

The isolated nucleic acid molecule of the present invention may be introduced into and expressed in any cell, for example a plant cell, fungal cell, insect cell, animal cell, yeast
30 cell or bacterial cell. Those skilled in the art will be aware of any modifications which are required to the codon usage or promoter sequences or other regulatory

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sequences, in order for expression to occur in such cells.

A further aspect of the invention provides a method of assaying for the presence or absence of a starch synthase isoenzyme or the copy number of a gene encoding same
5 in a plant, comprising contacting a biological sample derived from said plant with an isolated nucleic acid molecule derived from any one of SEQ ID NOS 1, 3, 5, 7, 9, 11-16, 37, or 38, or any one of SEQ ID NOS: 25 to 34, or a complementary nucleotide sequence thereto for a time and under conditions sufficient for hybridisation to occur and then detecting said hybridisation using a detection means.

10

The detection means according to this aspect of the invention is any nucleic acid based hybridisation or amplification reaction.

The hexaploid nature of wheat prevents the straightforward identification of starch
15 synthase allelic variants by hybridisation using the complete starch synthase-encoding sequence, because the similarities between the various alleles generally results in significant cross-hybridisation. Accordingly, sequence-specific hybridisation probes are required to distinguish between the various alleles. Similarly, wherein PCR is used to amplify specific allelic variants of a starch synthase gene, one or more sequence-
20 specific amplification primers are generally required. As will be apparent from the amino acid sequence comparisons provided herein, such as in Figures 3 and 13, non-conserved regions of particular wheat starch synthase polypeptides are particularly useful for the design of probes and primers that are capable of distinguishing between one or more starch synthase polypeptide isoenzyme or allelic variant. The present
25 invention clearly contemplates the design of such probes and primers based upon the sequence comparisons provided herein.

In the performance of this embodiment of the present invention, the present inventors particularly contemplate the identification of wheat starch synthase null alleles or
30 alternatively, mutations wherein specific amino acids are inserted or deleted or substituted, compared to one or more of the wheat SSII or SSIII alleles disclosed

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herein. Such null alleles and other allelic variants are readily identifiable using PCR screening which employs amplification primers based upon the nucleotide and amino acid sequences disclosed herein for SSII and/or SSIII. Once identified, the various mutations can be stacked or pyramided into one or more new wheat lines, such as by
5 introgression and/or standard plant breeding and/or recombinant approaches (eg. transformation, transfection, etc) thereby producing a novel germplasm which exhibits altered starch properties compared to existing lines. DNA markers based upon the nucleotide and amino acid sequences disclosed herein for SSII and/or SSIII can be employed to monitor the stacking of genes into the new lines and to correlate the
10 presence of particular genes with starch phenotypes of said lines.

In this regard, a significant advantage conferred by the present invention is the design of new DNA markers that reveal polymorphisms such as, for example, length polymorphisms, restriction site polymorphisms, and single nucleotide polymorphisms,
15 amongst others, between wheat starch synthases and, in particular, between wheat GBSS and/or SSI and/or SSII and/or SSIII, or between allelic variants of one or more of said starch synthases, that can be used to identify the three genomes of hexaploid wheats (i.e., the A, B and D genomes).

20 Preferably, such DNA markers are derived from the intron region of a starch synthase gene disclosed herein, more preferably the wheat SSII and/or the wheat SSIII gene. Those skilled in the art will be aware that such regions generally have a higher degree of variation than in the protein-encoding regions and, as a consequence, are particularly useful in identifying specific allelic variants of a particular gene, such as
25 allelic variants contained in any one of the three wheat genomes, or alternatively or in addition, for the purpose of distinguishing between wheat GBSS, SSI, SSII or SSIII genes.

A further approach contemplated by the present inventors is the design of unique
30 isoenzyme-specific and/or allele-specific peptides based upon the amino acid sequence disclosed herein as SEQ ID NOS: 25 and/or SEQ ID NO: 4 and/or SEQ ID

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NO: 6 and/or SEQ ID NO: 8 and/or SEQ ID NO: 10, which peptides are then used to produce polyclonal or monoclonal antibodies by conventional means. Alternatively, the genes encoding these polypeptides or unique peptide regions thereof can be introduced in an expressible format into an appropriate prokaryotic or eukaryotic
5 expression system, where they can be expressed to produce the isoenzyme-specific and/or allele-specific peptides for antibody production. Such antibodies may also be used as markers for the purpose of both identifying parental lines and germplasms and monitoring the stacking of genes in new lines, using conventional immunoassays such as, for example, ELISA and western blotting.

10

A further aspect of the present invention utilises the above-mentioned nucleic acid based assay method in the breeding and/or selection of plants which express or do not express particular starch synthase isoenzymes or alternatively, which express a particular starch synthase isoenzyme at a particular level in one or more plant tissues.

15 This aspect clearly extends to the selection of transformed plant material which contains one or more of the isolated nucleic acid molecules of the present invention.

Yet another aspect of the present invention provides for the expression of the nucleic acid molecule of the present invention in a suitable host (e.g. a prokaryote or
20 eukaryote) to produce full length or non-full length recombinant starch synthase gene products.

Hereinafter the term "starch synthase gene product" shall be taken to refer to a recombinant product of a starch synthase gene of the present invention.

25

Preferably, the recombinant starch synthase gene product comprises an amino acid sequence having the catalytic activity of a starch synthase polypeptide or a functional mutant, derivative part, fragment, or analogue thereof.

30 In a particularly preferred embodiment of the invention, the recombinant starch synthase gene product is selected from the following:

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- (i) a wheat starch synthase II (wSSII) polypeptide, protein or enzyme or functional subunit thereof which comprises an amino acid sequence which is at least about 85% identical overall to an amino acid sequence set forth in any one of SEQ ID NOS: 2, 4, or 6;
- 5 (ii) a wheat starch synthase III (wSSIII) polypeptide, protein or enzyme or functional subunit thereof which comprises an amino acid sequence which is at least about 85% identical overall to an amino acid sequence set forth in any one of SEQ ID NOS: 8 or 10; and
- (iii) a wheat starch synthase polypeptide, protein or enzyme or functional subunit thereof which comprises a conserved amino acid sequence having at least 25% identity to an amino acid sequence selected from the group consisting of:
- 10 (a) KVGGLGDVVTs;
(b) GHTVEVILPKY;
(c) HDWSSAPVAWLYKEHY;
(d) GILNGIDPDIWDPYTD;
(e) DVPIVGIITRLTAQKG;
(f) NGQVVLLGSA;
(g) AGSDFIIVPSIFEPCGLTQLVAMRYGS;
- 15 (h) TGGLVDTV; (i) a wheat starch synthase II (wSSII) polypeptide, protein or enzyme or functional subunit thereof which comprises an amino acid sequence which is at least about 85% identical overall to an amino acid sequence set forth in any one of SEQ ID NOS: 2, 4, or 6;
- 25 (ii) a wheat starch synthase III (wSSIII) polypeptide, protein or enzyme or functional subunit thereof which comprises an amino acid sequence which is at least about 85% identical overall to an amino acid sequence set forth in any one of SEQ ID NOS: 8 or 10;
- 30 (iii) a wheat starch synthase polypeptide, protein or enzyme or functional subunit thereof which comprises a conserved amino acid sequence having at

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least 25% identity to an amino acid sequence selected from the group consisting of:

- (a) KVGGLGDVVTS;
- (b) GHTVEVILPKY;
- 5 (c) HDWSSAPVAWLYKEHY;
- (d) GILNGIDPDIWDPYTD;
- (e) DVPIVGIIITRLTAQKG;
- (f) NGQVVLLGSA;
- (g) AGSDFIIVPSIFPCGLTQLVAMRYGS; and
- 10 (h) TGGLVDTV;
- (i) KTGGLGDVAGA;
- (j) GHRVMVVVPRY;
- (k) NDWHTALLPVYLKAYY;
- (l) GIVNGIDNMEWNPEVD;
- 15 (m) DVPLLGFIGRLDGQKG;
- (n) DVQLVMLGTG;
- (o) AGADALLMPSRF(E/V)PCGLNQLYAMAYGT; and
- (p) VGG(V/L)RDTV.

20 Accordingly, the present invention clearly extends to homologues, analogues and derivatives of the amino acid sequences set forth herein as SEQ ID NOS: 2, 4, 6, 8 and 10.

In the present context, "homologues" of an amino acid sequence refer to those
25 polypeptides, enzymes or proteins which have a similar catalytic activity to the amino acid sequences described herein, notwithstanding any amino acid substitutions, additions or deletions thereto. A homologue may be isolated or derived from the same or another plant species as the species from which the polypeptides of the invention are derived.

30

"Analogues" encompass polypeptides of the invention notwithstanding the occurrence

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of any non-naturally occurring amino acid analogues therein.

"Derivatives" include modified peptides in which ligands are attached to one or more of the amino acid residues contained therein, such as carbohydrates, enzymes, proteins, polypeptides or reporter molecules such as radionuclides or fluorescent compounds. Glycosylated, fluorescent, acylated or alkylated forms of the subject peptides are particularly contemplated by the present invention. Additionally, derivatives of an amino acid sequence described herein which comprises fragments or parts of the subject amino acid sequences are within the scope of the invention, as are homopolymers or heteropolymers comprising two or more copies of the subject polypeptides. Procedures for derivatizing peptides are well-known in the art.

Substitutions encompass amino acid alterations in which an amino acid is replaced with a different naturally-occurring or a non-conventional amino acid residue. Such substitutions may be classified as "conservative", in which an amino acid residue contained in a starch synthase gene product is replaced with another naturally-occurring amino acid of similar character, for example Gly↔Ala, Val↔Ile↔Leu, Asp↔Glu, Lys↔Arg, Asn↔Gln or Phe↔Trp↔Tyr.

Substitutions encompassed by the present invention may also be "non-conservative", in which an amino acid residue which is present in a starch synthase gene product described herein is substituted with an amino acid with different properties, such as a naturally-occurring amino acid from a different group (eg. substituted a charged or hydrophobic amino acid with alanine), or alternatively, in which a naturally-occurring amino acid is substituted with a non-conventional amino acid.

Non-conventional amino acids encompassed by the invention include, but are not limited to those listed in Table 2.

Amino acid substitutions are typically of single residues, but may be of multiple residues, either clustered or dispersed.

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Amino acid deletions will usually be of the order of about 1-10 amino acid residues, while insertions may be of any length. Deletions and insertions may be made to the N-terminus, the C-terminus or be internal deletions or insertions. Generally, insertions within the amino acid sequence will be smaller than amino- or carboxy-terminal fusions and of the order of 1-4 amino acid residues.

A homologue, analogue or derivative of a starch synthase gene product as referred to herein may readily be made using peptide synthetic techniques well-known in the art, such as solid phase peptide synthesis and the like, or by recombinant DNA manipulations. Techniques for making substituent mutations at pre-determined sites using recombinant DNA technology, for example by M13 mutagenesis, are also well-known. The manipulation of nucleic acid molecules to produce variant peptides, polypeptides or proteins which manifest as substitutions, insertions or deletions are well-known in the art.

15

The starch synthase gene products described herein may be derivatized further by the inclusion or attachment thereto of a protective group which prevents, inhibits or slows proteolytic or cellular degradative processes. Such derivatization may be useful where the half-life of the subject polypeptide is required to be extended, for example to increase the amount of starch produced in the endosperm or alternatively, to increase the amount of protein produced in a bacterial or eukaryotic expression system. Examples of chemical groups suitable for this purpose include, but are not limited to, any of the non-conventional amino acid residues listed in Table 2, in particular a D-stereoisomer or a methylated form of a naturally-occurring amino acid listed in Table 1. Additional chemical groups which are useful for this purpose are selected from the list comprising aryl or heterocyclic N-acyl substituents, polyalkylene oxide moieties, desulphatohirudin muteins, alpha-muteins, alpha-aminophosphonic acids, water-soluble polymer groups such as polyethylene glycol attached to sugar residues using hydrazone or oxime groups, benzodiazepine dione derivatives, glycosyl groups such as beta-glycosylamine or a derivative thereof, isocyanate conjugated to a polyol functional group or polyoxyethylene polyol capped with diisocyanate, amongst others. Similarly, a starch synthase gene product or a homologue, analogue or derivative

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thereof may be cross-linked or fused to itself or to a protease inhibitor peptide, to reduce susceptibility of said molecule to proteolysis.

In a particularly preferred embodiment, the percentage similarity to in any one of SEQ
5 ID NOS: 2, 4, 6, 8 or 10 is at least about 90%, more preferably at least about 95%,
even more preferably at least about 97% and even more preferably at least about
98%, or about 99% or 100%.

In a related embodiment, the present invention provides a "sequencably pure" form of
10 the amino acid sequence described herein. "Sequencably pure" is hereinbefore
described as substantially homogeneous to facilitate amino acid determination.

In a further related embodiment, the present invention provides a "substantially
homogeneous" form of the subject amino acid sequence, wherein the term
15 "substantially homogeneous" is hereinbefore defined as being in a form suitable for
interaction with an immunologically interactive molecule. Preferably, the polypeptide
is at least 20% homogeneous, more preferably at least 50% homogeneous, still more
preferably at least 75% homogeneous and yet still more preferably at least about 95-
100% homogenous, in terms of activity per microgram of total protein in the protein
20 preparation.

To produce the recombinant polypeptide of the present invention, the coding region
of a starch synthase gene described herein or a functional homologue, analogue or
derivative thereof is placed operably in connection with a promoter sequence in the
25 sense orientation, such that a starch synthase gene product is capable of being
expressed under the control of said promoter sequence.

In the present context, the term "in operable connection with" means that expression
of the isolated nucleotide sequence is under the control of the promoter sequence with
30 which it is connected, regardless of the relative physical distance of the sequences
from each other or their relative orientation with respect to each other.

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Reference herein to a "promoter" is to be taken in its broadest context and includes the transcriptional regulatory sequences of a classical genomic gene, including the TATA box which is required for accurate transcription initiation, with or without a CCAAT box sequence and additional regulatory elements (i.e. upstream activating sequences, enhancers and silencers) which alter gene expression in response to developmental and/or external stimuli, or in a tissue-specific manner. A promoter is usually, but not necessarily, positioned upstream or 5', of a structural gene, the expression of which it regulates. Furthermore, the regulatory elements comprising a promoter are usually positioned within 2 kb of the start site of transcription of the gene.

10

In the present context, the term "promoter" is also used to describe a synthetic or fusion molecule, or derivative which confers, activates or enhances expression of a structural gene or other nucleic acid molecule, particularly in a plant cell and more preferably in a wheat plant or other monocotyledonous plant cell, tissue or organ. Preferred promoters may contain additional copies of one or more specific regulatory elements, to further enhance expression and/or to alter the spatial expression and/or temporal expression. For example, regulatory elements which confer copper inducibility may be placed adjacent to a heterologous promoter sequence, thereby conferring copper inducibility on the expression of said molecule.

20

Those skilled in the art will be aware that in order to obtain optimum expression of the starch synthase gene of the present invention, it is necessary to position said gene in an appropriate configuration such that expression is controlled by the promoter sequence. Promoters are generally positioned 5' (upstream) to the genes that they control. In the construction of heterologous promoter/structural gene combinations it is generally preferred to position the promoter at a distance from the gene transcription start site that is approximately the same as the distance between that promoter and the gene it controls in its natural setting, i.e., the gene from which the promoter is derived. As is known in the art, some variation in this distance can be accommodated without loss of promoter function. Similarly, the preferred positioning of a regulatory sequence element with respect to a heterologous gene to be placed under its control is defined by the positioning of the element in its natural setting, i.e., the genes from

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which it is derived. Again, as is known in the art, some variation in this distance can also occur.

Examples of promoters suitable for expressing the starch synthase gene of the present invention include viral, fungal, bacterial, animal and plant derived promoters capable of functioning in prokaryotic or eukaryotic cells. Preferred promoters are those capable of regulating the expression of the subject starch synthase genes in plants cells, fungal cells, insect cells, yeast cells, animal cells or bacterial cells, amongst others. Particularly preferred promoters are capable of regulating expression of the subject nucleic acid molecules in monocotyledonous plant cells. The promoter may regulate the expression of the said molecule constitutively, or differentially with respect to the tissue in which expression occurs or, with respect to the developmental stage at which expression occurs, or in response to external stimuli such as physiological stresses, or plant pathogens, or metal ions, amongst others.

15

Accordingly, strong constitutive promoters are particularly preferred for the purposes of the present invention.

Examples of preferred promoters include the bacteriophage T7 promoter, bacteriophage T3 promoter, SP6 promoter, *lac* operator-promoter, *tac* promoter, SV40 late promoter, SV40 early promoter, RSV-LTR promoter, CMV IE promoter, CaMV 35S promoter, SCSV promoter, SCBV promoter and the like.

Particularly preferred promoters operable in plant cells include, for example the CaMV 35S promoter, and the SCBV promoter. Those skilled in the art will readily be aware of additional promoter sequences other than those specifically described.

In a particularly preferred embodiment, the promoter may be derived from a genomic starch synthase gene. Preferably, the promoter sequence comprises nucleotide sequences that are linked *in vivo* to nucleotide sequences set forth in any one of SEQ ID NOs: 1, 3, 5, 7, 9, 11-16, 37, or 38. By "linked *in vivo*" means that the promoter is present in its native state in the genome of a wheat plant where it controls expression

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of the starch synthase gene of the present invention.

Conveniently, genetic constructs are employed to facilitate expression of a starch synthase genetic sequence of the present invention or a functional derivative, part, 5 homologue, or analogue thereof. To produce a genetic construct, the starch synthase gene of the invention is inserted into a suitable vector or episome molecule, such as a bacteriophage vector, viral vector or a plasmid, cosmid or artificial chromosome vector which is capable of being maintained and/or replicated and/or expressed in the host cell, tissue or organ into which it is subsequently introduced. The said genetic 10 construct comprises the subject nucleic acid molecule placed operably under the control of a promoter sequence and optionally, a terminator sequence.

The term "terminator" refers to a DNA sequence at the end of a transcriptional unit which signals termination of transcription. Terminators are 3'-non-translated DNA 15 sequences containing a polyadenylation signal, which facilitates the addition of polyadenylate sequences to the 3'-end of a primary transcript. Terminators active in bacteria, yeasts, animal cells and plant cells are known and described in the literature. They may be isolated from bacteria, fungi, viruses, animals and/or plants.

20 Examples of terminators particularly suitable for use in expressing the nucleic acid molecule of the present invention in plant cells include the nopaline synthase (NOS) gene terminator of *Agrobacterium tumefaciens*, the terminator of the Cauliflower mosaic virus (CaMV) 35S gene, and the *zein* gene terminator from *Zea mays*.

25 Genetic constructs will generally further comprise one or more origins of replication and/or selectable marker gene sequences.

The origin of replication can be functional in a bacterial cell and comprise, for example, the pUC or the ColE1 origin. Alternatively, the origin of replication is operable in a 30 eukaryotic cell, tissue and more preferably comprises the 2 micron (2 μ m) origin of replication or the SV40 origin of replication.

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As used herein, the term "selectable marker gene" includes any gene which confers a phenotype on a cell in which it is expressed to facilitate the identification and/or selection of cells which are transfected or transformed with a genetic construct of the invention or a derivative thereof.

5

Suitable selectable marker genes contemplated herein include the ampicillin-resistance gene (Amp^r), tetracycline-resistance gene (Tc^r), bacterial kanamycin-resistance gene (Kan^r), is the zeocin resistance gene (Zeocin is a drug of bleomycin family which is trademark of InVitrogen Corporation), the *AURI-C* gene which confers resistance to the
10 antibiotic aureobasidin A, phosphinothricin-resistance gene, neomycin phosphotransferase gene (*nptII*), hygromycin-resistance gene, β -glucuronidase (GUS) gene, chloramphenicol acetyltransferase (CAT) gene, green fluorescent protein-encoding gene or the luciferase gene, amongst others. Those skilled in the art will be aware of other selectable marker genes useful in the performance of the present
15 invention and the subject invention is not limited by the nature of the selectable marker gene.

Usually, an origin of replication or a selectable marker gene suitable for use in bacteria is physically-separated from those genetic sequences contained in the genetic
20 construct which are intended to be expressed or transferred to a eukaryotic cell, or integrated into the genome of a eukaryotic cell.

Standard methods can be used to introduce genetic constructs into a cell, tissue or organ for the purposes of modulating gene expression. Particularly preferred methods
25 suited to the introduction of synthetic genes and genetic constructs comprising same to eukaryotic cells include liposome-mediated transfection or transformation, transformation of cells with attenuated virus particles or bacterial cells and standard procedures for the transformation of plant and animal cells, tissues, organs or organisms. Any standard means may be used for their introduction including cell
30 mating, transformation or transfection procedures known to those skilled in the art or described by Ausubel *et al.* (1992).

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In a further embodiment of the present invention, the starch synthase genes of the present invention and genetic constructs comprising same are adapted for integration into the genome of a cell in which it is expressed. Those skilled in the art will be aware that, in order to achieve integration of a genetic sequence or genetic construct into the genome of a host cell, certain additional genetic sequences may be required. In the case of plants, left and right border sequences from the T-DNA of the *Agrobacterium tumefaciens* Ti plasmid will generally be required.

The invention further contemplates increased starch and/or modified starch composition in transgenic plants expressing the nucleic acid molecule of the invention in the sense orientation such that the activity of one or more starch synthase isoenzymes is increased therein. By increasing the level of one or more starch synthase isoenzymes, the deposition of starch in the amyloplast or chloroplast is increased and/or a modified starch granule structure is produced and/or starch composition is modified and/or the amylose/amylopectin ratio is altered in the plant.

Wherein it is desired to increase the synthesis of a particular starch synthase isoenzyme in a plant cell, the coding region of a starch synthase gene is placed operably behind a promoter, in the sense orientation, such that said starch synthase is expressed under the control of said promoter sequence. In a preferred embodiment, the starch synthase genetic sequence is a starch synthase genomic sequence, cDNA molecule or protein-coding sequence.

Wherein it is desirable to reduce the level of a particular starch synthase isoenzyme in a plant cell, the nucleic acid molecule of the present invention can be expressed in the antisense orientation, as an antisense molecule or a ribozyme molecule, under the control of a suitable promoter.

Alternatively, the nucleic acid molecule of the present invention may also be expressed in the sense orientation, in the form of a co-suppression molecule, to reduce the level of a particular starch synthase isoenzyme in a plant cell. As will be known to those skilled in the art, co-suppression molecules that comprise inverted repeat sequences

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of a target nucleic acid molecule provide optimum efficiency at reducing expression of said target nucleic acid molecule and, as a consequence, the present invention clearly contemplates the use of inverted repeat sequences of any one or more of the starch synthase genetic sequences exemplified herein, or inverted repeat sequences of a
5 homologue, analogue or derivative of said starch synthase genetic sequences, to reduce the level of a starch synthase isoenzyme in a plant.

The expression of an antisense, ribozyme or co-suppression molecule comprising a starch synthase gene in a cell such as a plant cell, fungal cell, insect cell, animal cell,
10 yeast cell or bacterial cell, may also increase the availability of carbon as a precursor for a secondary metabolite other than starch (e.g. sucrose or cellulose). By targeting the endogenous starch synthase gene, expression is diminished, reduced or otherwise lowered to a level that results in reduced deposition of starch in the amyloplast or chloroplast and/or leads to modified starch granule structure and/or composition
15 and/or altered amylose/amylopectin ratio.

Accordingly, a further aspect of the present invention provides a method of modifying the starch content and/or starch composition of one or more tissues or organs of a plant, comprising expressing therein a sense molecule, antisense molecule, ribozyme
20 molecule, co-suppression molecule, or gene-targeting molecule having at least about 85% nucleotide sequence identity to any one of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37, or 38, or a complementary nucleotide sequence thereto for a time and under conditions sufficient for the enzyme activity of one or more starch synthase isoenzymes to be modified. This aspect of the invention clearly extends to the
25 introduction of the sense molecule, antisense molecule, ribozyme molecule, co-suppression molecule, or gene-targeting molecule to isolated plant cells, tissues or organs or organelles by cell fusion or transgenic means and the regeneration of intact plants therefrom.

30 Co-suppression is the reduction in expression of an endogenous gene that occurs when one or more copies of said gene, or one or more copies of a substantially similar

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gene are introduced into the cell, preferably in the form of an inverted repeat structure.

The present inventors have discovered that the genetic sequences disclosed herein are capable of being used to modify the level of starch when expressed, particularly when expressed in plants cells. Accordingly, the present invention clearly extends to the modification of starch biosynthesis in plants, in particular wheat or barley plants or a progenitor plant species, or a relative thereto such as the diploid *Triticum tauschii* or other diploid, tetraploid, aneuploid, polyploid, nullisomic, or a wheat/barley addition line, amongst others.

10

In particular, the present invention contemplates decreased starch production and/or modified starch composition in transgenic plants expressing the nucleic acid molecule of the invention in the antisense orientation or alternatively, expressing a ribozyme or co-suppression molecule comprising the nucleic acid sequence of the invention such that the activity of one or more starch synthase isoenzymes is decreased therein.

15

In the context of the present invention, an antisense molecule is an RNA molecule which is transcribed from the complementary strand of a nuclear gene to that which is normally transcribed to produce a "sense" mRNA molecule capable of being translated into a starch synthase polypeptide. The antisense molecule is therefore complementary to the mRNA transcribed from a sense starch synthase gene or a part thereof. Although not limiting the mode of action of the antisense molecules of the present invention to any specific mechanism, the antisense RNA molecule possesses the capacity to form a double-stranded mRNA by base pairing with the sense mRNA, which may prevent translation of the sense mRNA and subsequent synthesis of a polypeptide gene product.

25

Ribozymes are synthetic RNA molecules which comprise a hybridising region complementary to two regions, each of at least 5 contiguous nucleotide bases in the target sense mRNA. In addition, ribozymes possess highly specific endoribonuclease

30

activity, which autocatalytically cleaves the target sense mRNA. A complete description of the function of ribozymes is presented by Haseloff and Gerlach (1988) and contained in International Patent Application No. WO89/05852.

- 5 The present invention extends to ribozyme which target a sense mRNA encoding a native starch synthase gene product, thereby hybridising to said sense mRNA and cleaving it, such that it is no longer capable of being translated to synthesise a functional polypeptide product.
- 10 According to this embodiment, the present invention provides a ribozyme or antisense molecule comprising at least 5 contiguous nucleotide bases derived from any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37, or 38, or a complementary nucleotide sequence thereto or a homologue, analogue or derivative thereof, wherein said antisense or ribozyme molecule is able to form a hydrogen-bonded complex with a sense mRNA
- 15 encoding a starch synthase gene product to reduce translation thereof.

In a preferred embodiment, the antisense or ribozyme molecule comprises at least 10 to 20 contiguous nucleotides derived from any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37, or 38, or a complementary nucleotide sequence thereto or a homologue, analogue

20 or derivative thereof. Although the preferred antisense and/or ribozyme molecules hybridise to at least about 10 to 20 nucleotides of the target molecule, the present invention extends to molecules capable of hybridising to at least about 50-100 nucleotide bases in length, or a molecule capable of hybridising to a full-length or substantially full-length mRNA encoded by a starch synthase gene.

25

Those skilled in the art will be aware of the necessary conditions, if any, for selecting or preparing the antisense or ribozyme molecules of the invention.

It is understood in the art that certain modifications, including nucleotide substitutions

30 amongst others, may be made to the antisense and/or ribozyme molecules of the present invention, without destroying the efficacy of said molecules in inhibiting the expression of a starch synthase gene. It is therefore within the scope of the present

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invention to include any nucleotide sequence variants, homologues, analogues, or fragments of the said gene encoding same, the only requirement being that said nucleotide sequence variant, when transcribed, produces an antisense and/or ribozyme molecule which is capable of hybridising to a sense mRNA molecule which
5 encodes a starch synthase gene product.

Gene targeting is the replacement of an endogenous gene sequence within a cell by a related DNA sequence to which it hybridises, thereby altering the form and/or function of the endogenous gene and the subsequent phenotype of the cell. According
10 to this embodiment, at least a part of the DNA sequence defined by any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37, or 38 may be introduced into target cells containing an endogenous gene that encodes a particular starch synthase isoenzyme, thereby replacing said endogenous gene. According to this embodiment, the polypeptide product of the gene targeting molecule generally encodes a starch synthase
15 isoenzyme that possesses different catalytic activity to the polypeptide product of the endogenous gene, producing in turn modified starch content and/or composition in the target cell.

The present invention extends to genetic constructs designed to facilitate expression
20 of a sense molecule, an antisense molecule, ribozyme molecule, co-suppression molecule, or gene targeting molecule of the present invention. The requirements for expressing such molecules are similar to those for expressing a recombinant polypeptide as described *supra*.

25 The present invention further extends to the production and use of starches and proteins produced using the novel genes described herein. Modified starches produced by plants which have been selected using marker-assisted selection, or alternatively, produced by transgenic plants carrying the introduced starch synthase genes, are particularly suitable for use in food products, such as, for example, flour
30 and flour-based products, in particular those products selected from the group consisting of: flour-based sauce; leavened bread; unleavened bread; pasta, noodle; cereal; snack food; cake; and pastry. Modified proteins are also suitable for use in non-

food products, such as, for example, those non-food products selected from the group consisting of: films; coatings; adhesives; building materials; and packaging materials.

Additionally, starch hydrolysates or undegraded starches are both useful in industry and, as a consequence, the present invention is useful in applications relating to the use of both starch hydrolysates and undegraded starches. By "starch hydrolysates" is meant the glucose and glucan components that are obtainable by the enzymatic or chemical degradation of starch in chemical modifications and processes, such as fermentation.

10

Starch produced by plants expressing the sense, antisense, co-suppression, gene-targeting or ribozyme molecules of the present invention may exhibit modified viscosities and/or gelling properties of its glues when compared to starch derived from wild-type plants. Native starches produced by the performance of the inventive method are useful as an additive in the following: (i) foodstuffs, for the purpose of increasing the viscosity or gelling properties of food; (ii) in non-foodstuffs, such as an adjuvant or additive in the paper and cardboard industries, for retention or as a size filler, or as a solidifying substance or for dehydration, or film coating, amongst others; (iii) in the adhesive industry as pure starch glue, as an additive to synthetic resins and polymer dispersions, or as an extenders for synthetic adhesives; (iv) in the textile and textile care industries to strengthen woven products and reduce burring or to thicken dye pastes; (v) in the building industry, such as a binding agent in the production of gypsum plaster boards, or for the deceleration of the sizing process; (vi) in ground stabilization or for the temporary protection of ground particles against water in artificial earth shifting; (vii) as a wetting agent in plant protectants and fertilizers; (viii) as a binding agent in drugs, pharmaceuticals and medicated foodstuff such as vitamins, etc; (ix) as an additive in coal and briquettes; (xi) as a flocculent in the processing of coal ore and slurries; (xii) as a binding agent in casting processes to increase flow resistance and improve binding strength; and (xiii) to improve the technical and optical quality of rubber and plastic products. Additional applications are not excluded.

30

A further aspect of the present invention provides an isolated promoter that is operable

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in the endosperm of a monocotyledonous plant cell, tissue or organ, and preferably in the endosperm of a monocotyledonous plant cell, tissue or organ. According to this embodiment, it is preferred that the promoter is derived from a starch synthase gene of the present invention, such as a promoter that is linked *in vivo* to any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37, or 38, or a complementary nucleotide sequence thereto.

In a particularly preferred embodiment, the promoter comprises a nucleotide sequence derivable from the 5'-upstream region of SEQ ID NO: 11 or SEQ ID NO: 37 or SEQ ID NO: 38, or a complementary nucleotide sequence thereto, and more preferably comprises nucleotides 1 to about 287 of SEQ ID NO: 11, or nucleotides 1 to about 1416 of SEQ ID NO: 37, or nucleotides 1 to about 973 of SEQ ID NO: 38, or a complementary nucleotide sequence thereto. The present invention clearly extends to promoter sequences that comprise further nucleotide sequences in the region upstream of the stated nucleotide sequence that are linked *in vivo* to said nucleotide sequence in the wheat genome.

In a related embodiment, the promoter sequence of the present invention will further comprise an exon sequence derived from a starch synthase gene, such as, for example, an intron I sequence described herein, or a complementary nucleotide sequence thereto. Those skilled in the art will be aware that the inclusion of such nucleotide sequences may increase the expression of a heterologous structural gene, the expression of which is controlled thereby. Preferred intron I sequences include, for example, nucleotide sequences in the region of about position 1744 to about 1847 of SEQ ID NO: 37, and/or about position 1100 to about position 2056 of SEQ ID NO: 38. Additional sequences comprising intron/exon junction boundary sequences which are readily determined by those skilled in the art are not excluded.

The present invention further extends to the expression of any structural gene operably under the control of the starch synthase promoter sequence exemplified herein or a functional homologue, analogue or derivative of said promoter sequence.

As with other embodiments described herein for expression in cells, a genetic construct may be employed to effect said expression and the present invention clearly extends to said genetic constructs.

- 5 The polypeptide encoded by the structural gene component may be a reporter molecule which is encoded by a gene such as the bacterial β -glucuronidase gene or chloramphenicol acetyltransferase gene or alternatively, the firefly luciferase gene. Alternatively, wherein it is desirable to alter carbon partitioning within the endosperm, the polypeptide may be an enzyme of the starch sucrose biosynthetic pathways.
- 10 Preferably, the promoter sequence is used to regulate the expression of one or more of the starch synthase genes of the present invention or a sense, antisense, ribozyme, co-suppression or gene-targetting molecule comprising or derived from same.

Recombinant DNA molecules carrying the aforesaid nucleic acid molecule of the present invention or a sense, antisense, ribozyme, gene-targetting or co-suppression molecule and/or genetic construct comprising same, may be introduced into plant tissue, thereby producing a "transgenic plant", by various techniques known to those skilled in the art. The technique used for a given plant species or specific type of plant tissue depends on the known successful techniques. Means for introducing recombinant DNA into plant tissue include, but are not limited to, transformation (Paszowski *et al.*, 1984), electroporation (Fromm *et al.*, 1985), or microinjection of the DNA (Crossway *et al.*, 1986), or T-DNA-mediated transfer from *Agrobacterium* to the plant tissue. Representative T-DNA vector systems are described in the following references: *Ali et al.* (1985); Herrera-Estrella *et al.* (1983a, b); Herrera-Estrella *et al.* (1985). Once introduced into the plant tissue, the expression of the introduced gene may be assayed in a transient expression system, or it may be determined after selection for stable integration within the plant genome. Techniques are known for the *in vitro* culture of plant tissue, and in a number of cases, for regeneration into whole plants. Procedures for transferring the introduced gene from the originally transformed plant into commercially useful cultivars are known to those skilled in the art.

In general, plants are regenerated from transformed plant cells or tissues or organs on

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hormone-containing media and the regenerated plants may take a variety of forms, such as chimeras of transformed cells and non-transformed cells; clonal transformants (e.g., all cells transformed to contain the expression cassette); grafts of transformed and untransformed tissues (e.g., a transformed root stock grafted to an untransformed scion in citrus species). Transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plants may be selfed to give homozygous second generation (or T2) transformed plants, and the T2 plants further propagated through classical breeding techniques.

10

Accordingly, a still further aspect of the present invention contemplates a transgenic plant comprising an introduced sense molecule, antisense molecule, ribozyme molecule, co-suppression molecule, or gene-targeting molecule having at least about 85% nucleotide sequence identity to any one of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11-16, 37, or 38, or a complementary nucleotide sequence thereto or a genetic construct comprising same. The present invention further extends to those plant parts, propagules and progeny of said transgenic plant or derived therefrom, the only requirement being that said propagules and progeny also carry the introduced nucleic acid molecule(s).

20

The present invention is further described by reference to the following non-limiting examples.

EXAMPLE 1

Plant material

25 Genetic stocks of hexaploid bread wheat *Triticum aestivum* cv. Chinese Spring with various chromosome additions and deletions were kindly supplied by Dr E. Lagudah (CSIRO Plant Industry, Canberra) and derived from stocks described in Sears and Miller (1985). The hexaploid (*Triticum aestivum*) wheats cv Gabo and cv Wyuna were grown in controlled growth cabinet conditions (18°C day and 13°C night, with a photoperiod of 16 h). Wheat leaves and florets prior to anthesis, and endosperm were collected over the grain filling period, immediately frozen in liquid nitrogen and stored

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at -80°C until required.

EXAMPLE 2

Gel Electrophoresis, Antibodies and Immunoblotting

- 5 Monoclonal antibodies against the Sgp-1 proteins, and their use in the immunoblotting of SDS-PAGE gels have been described previously (Rahman *et al.*, 1995).

EXAMPLE 3

Preparation of total RNA from wheat

- 10 Total RNA was isolated from the leaf, floret and endosperm tissues of wheat essentially as described by Higgins *et al.* (1976) or Rahman *et al.* (1998). RNA was quantified by UV absorption and by separation in 1.4% (w/v) agarose-formaldehyde gels which were then visualised under UV light after staining with ethidium bromide.

EXAMPLE 4

Construction and screening of cDNA libraries

- 15 A first cDNA library, an expression cDNA library of wheat endosperm, was constructed from mRNA isolated from wheat cv Chinese Spring. RNA from 5, 7, 9, 11 and 13 days after anthesis was pooled and random primers were used for the first strand of cDNA synthesis. Monoclonal antibodies against 100 -105 kDa proteins in wheat starch granules (Rahman *et al.*, 1995) were used for immunoscreening of the expression cDNA library.

- A second cDNA library was constructed from the endosperm mRNA of the hexaploid
25 *Triticum aestivum* cultivar Wyuna, 8 - 12 days after anthesis, as described by Rahman *et al.* (1997). This library was screened with a 85-bp cDNA fragment, wSSIIP1, which was obtained by immunoscreening of the expression cDNA library as described above. The wSSIIP1 probe corresponded to nucleotide positions 988 to 1072 of wSSIIB (SEQ ID NO:1) at the hybridisation conditions as described earlier (Rahman *et al.*, 1998).

30

A third cDNA library was constructed from RNA from the endosperm of the hexaploid

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Triticum aestivum cultivar Rosella as described by Rahman *et al.* (1997). This library was screened with a 347-bp cDNA fragment, wSSIIIp1 for the first screening, and a 478-bp cDNA fragment wSSIIIp3 for the second screening using the hybridisation conditions described herein.

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EXAMPLE 5

Construction and screening of *Triticum tauschii* genomic library

The genomic library used in this study, prepared from *Triticum tauschii*, var strangulata, (Accession Number CPI 110799), has been described in Rahman *et al.*,
10 (1997). Of all the accessions of *T. tauschii* surveyed, DNA marker analysis suggests that the genome of CPI 110799 is the most closely related to the D genome of hexaploid wheat (Lagudah *et al.*, 1991).

Hybridisations were carried out in 25% formamide, 6 x SSC, 0.1% SDS at 42°C for 16
15 hours, then filters were washed 3 times using 2 x SSC containing 0.1% SDS at 65°C for 1 hour per wash.

For the isolation of a genomic wSSII clone, the probe comprised the PCR-derived DNA fragment wSSIIp2 and positive-hybridising plaques were digested using the restriction
20 enzyme *Bam*HI, separated on a 1% agarose gel, transferred to nitrocellulose membrane and hybridised to probe wSSIIp4 comprising nucleotides 1 to 367 of the wSSIIA cDNA clone, using the conditions described by Rahman *et al.* (1997).

For the isolation of a genomic wSSIII clone, plaques hybridising to the PCR-derived
25 DNA fragment wSSIIIp1 from clone wSSIII.B3 (i.e. nucleotides 3620 to 3966 of SEQ ID NO:7) were selected and re-screened until plaque-purified.

EXAMPLE 6

DNA sequencing and analysis

30 DNA sequencing was performed using the automated ABI system with dye terminators as described by the manufacturers. DNA sequences were analysed using the GCG

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suite of programs (Devereaux *et al.*, 1984).

EXAMPLE 7

DNA and RNA analysis

5 DNA was isolated and analysed as previously described (Maniatis *et al.*, 1982; Rahman *et al.*, 1998). Approximately 20 μ g of DNA was digested with restriction enzymes *Bam*HI, *Dra*I and *Eco*RI, separated on a 1% agarose gel and transferred to reinforced nitrocellulose membranes (BioRad) and hybridised with 32 P-labelled DNA probe, either wSSIIIp1, corresponding to nucleotides 3620 to 3966 of the wheat SSIII
10 gene, or alternatively, with the entire wSSII cDNA clone. DNA fragment probes were labelled with the Rapid Multiprime DNA Probe Labelling Kit (Promega).

The hybridisation and wash conditions were performed as described in Rahman *et al.* (1997). For RNA analysis, 10 μ g of total RNA was separated in a 1.4% agarose-
15 formaldehyde gel and transferred to a Hybond N+ membrane (Amersham), and hybridised with cDNA probe at 42°C as previously described by Khandjian *et al.*, (1987) or Rahman *et al.*, (1998). After washing for 30 minutes at 65°C with 2x SSC, 0.1% SDS; followed by three washes of 40 minutes at 65°C with 0.2x SSC, 1% SDS, the membranes were visualised by overnight exposure at -80°C with Kodak MR X-ray
20 film.

EXAMPLE 8

Expression of wheat Sgp-1 polypeptides in the wheat endosperm

The development and use of monoclonal antibodies to the Sgp-1 proteins has been
25 described previously (Rahman *et al.*, 1995). These antibodies were used by the present inventors to characterise the expression and localisation of the Sgp-1 proteins.

The proteins found in the matrix of the wheat starch granule are shown in Figure 1, lane 1. The remaining lanes show an immunoblot of proteins from the soluble phase
30 (Figure 1; lanes 2-4) and the starch granule (Figure 1; lanes 5-7), respectively, following SDS-PAGE. In addition to cross-reactivity with the 100-105 kDa proteins, a

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weak cross-reaction with a 50 kDa protein in both the granule and the soluble fractions were observed (Figure 1). The Sgp-1 polypeptides are present in the starch granule throughout endosperm development (Figure 1; lanes 5-7, also see Rahman *et al.*, 1995). However, as the endosperm matures, there is a reduction in the amount of Sgp-1 protein found in the soluble fraction. Lane 4 shows that by 25 days after anthesis, the level of these proteins in the soluble fraction is substantially reduced. This observation is consistent with previous results from Rahman *et al.*, (1995), who suggested that the Sgp-1 proteins were exclusively granule bound based on studies of granules from endosperm in mid-late stages endosperm development, however, these results suggest that the partitioning of these proteins between the granule and the soluble phase changes during development.

EXAMPLE 9

Isolation of cDNA clones encoding wheat starch synthase II (wSSII) proteins

Monoclonal antibodies against Sgp-1 polypeptides (Rahman *et al.*, 1995) were used to probe the expression library described in Example 4 (i.e. the first cDNA library). Three immunoreactive plaques were identified and sequenced. One clone, designated wSSIIp1, contained an 85-bp cDNA insert with homology to maize SSIIa (Harn *et al.*, 1998).

20

DNA from the wSSIIp1 clone was used as a probe in the hybridisation screening of the second cDNA library, prepared from *Triticum aestivum* cultivar Wyuna endosperm RNA as described in Example 4. Ten hybridising cDNA clones were selected and sequenced. On the basis of the DNA sequences obtained, the 10 cDNA clones can be classified into three groups. Group 1 contains 7 cDNA clones, group 2 contains 2 cDNA clones and group 3 contains 1 cDNA clone.

The longest clone from group 1 (designated wSSIIb) is 2939 bp in length (SEQ ID NO:1) and encodes a 798 -amino acid polypeptide in the region from nucleotide position 176 to nucleotide position 2569 (SEQ ID NO:2).

30

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The longest clone from group 2 (designated wSSIIA) is 2842 bp in length (SEQ ID NO:3) and encodes a 799 -amino acid polypeptide in the region from nucleotide position 89 to nucleotide position 2485 (SEQ ID NO:4).

- 5 The cDNA from group 3 is a partial cDNA clone (designated wSSIID), which is 2107 bp in length (SEQ ID NO:5) and encodes a 597 -amino acid polypeptide in the region from nucleotide position 1 to nucleotide position 1791 (SEQ ID NO:6). The encoded polypeptide is approximately a 200 amino acid residues shorter than that of polypeptides encoded by longest clones of group 1 or 2 clones, respectively (Figure 10 2).

Comparison of the three cDNA clones, wSSIIB, wSSIIA and wSSIID shows that they share 95.7% to 96.6% identity at the amino acid level, with variation at 44 amino acid positions between the three sequences (Figure 3). Of the 44 amino acid changes between these sequences, 31 changes occur in the N-terminal region (residues 1 to 300), 10 changes occur in the central region (residues 301 to 729) and 3 changes occur in the C-terminal region (residues 730 to 799). The wSSIIA polypeptide (799 amino acid residues) and wSSIIB polypeptide (798 amino acid residues) sequences differ in length by a single amino acid residue, due to the deletion of Asp-69 from the 20 wSSIIB polypeptide sequence.

A comparison of the nucleotide sequences of the wSSIA, wSSIIB and wSSIID cDNA clones with the nucleotide sequence of the wSSIIP1 cDNA obtained by immunoscreening confirms that the wSSIIP1 sequence is found in each cDNA (Figure 25 3). The peptide encoded by the wSSIIP1 cDNA clone corresponds to amino acid residues in the region from residue 272 to residue 298 of the wSSIIA polypeptide, and to amino acid residues in the region from residue 271 to residue 297 of the wSSIIB polypeptide (see Figure 3). Thus, the peptide epitope encoded by wSSIIP1 that reacts with the anti-Sgp-1 monoclonal antibodies can therefore be localised to this region of 30 the wSSIIA and wSSIIB polypeptides and to the corresponding region of the wSSIID polypeptide.

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Notwithstanding that a region having about 63% amino acid sequence identity to the peptide epitope encoded by clone wSSIIP1 is found in the maize SSIIa polypeptide (Figure 3), the degree of amino acid conservation between maize and wheat sequences in this region of the polypeptide is insufficient for immunological cross-reactivity to occur between these species using the monoclonal antibodies to the wheat Sgp-1 proteins described by Rahman *et al.* (1995). Additionally, this peptide epitope is not found in granule-bound starch synthases, SSI, or SSIII (data not shown).

The wSSIIB cDNA (SEQ ID NO:1) encodes an amino acid sequence comprising the peptide motif AAGKKDAGID (SEQ ID NO: 18) between residues 60 and 69 of SEQ ID NO:2 (Figure 3) which, with the exception of the second residue, is identical to the N-terminal of the 100 kDa (A^T_LGKKDAGID: SEQ ID NOS:19 and 20) protein (Sgp-B1) from the wheat starch granule (note that the sequence given in Rahman *et al.*, 1995 (A^T_LGKKDAL: SEQ ID NOS: 21 and 22) has been revised following further amino acid sequence analysis).

The wSSIa cDNA clone (SEQ ID NO:3) encodes an amino acid sequence comprising the peptide motif AAGKKDARVDDDA (SEQ ID NO: 23) at residues 60 to 73 of SEQ ID NO:4, which is about 66% identical to the N-terminal amino acid sequence (i.e. ALGKKDAGIVDGA: SEQ ID NO: 24) of the 104 kDa and 105 kDa starch granule proteins, Sgp-D1 and Sgp-A1 respectively, as determined by sequence analysis of isolated protein (Rahman *et al.*, 1995).

Furthermore, Takaoka *et al.* (1997) reported the amino acid sequences of 3 polypeptides obtained from sequencing starch granule proteins derived from the Sgp-1 proteins. Peptide 3 described by Takaoka *et al.* (1997) corresponds to amino acid residues 378 to 387 of the amino acid sequence of the wSSIa cDNA (SEQ ID NO:4; Figure 3). Peptides 1 and 2 described by Takaoka *et al.* (1997) could not be detected in the amino acid sequences of the wSSII cDNA clones of the present invention, however peptide 1 of Takaoka *et al.* (1997) can be found in the amino acid sequences of SSI from maize, rice, wheat and potato (data not shown).

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Denyer *et al.* (1995) demonstrated that the Sgp-1 proteins possess starch synthase activity and, as a consequence, the wSSIIB, wSSIA and wSSIID cDNA clones encode starch synthase enzymes that are differentially expressed in a developmentally-regulated manner in both the soluble and granule-bound fractions of the endosperm (Figure 1). Based on the nomenclature suggested by Harn *et al.* (1998), it is appropriate to describe the Sgp-1 proteins as "starch synthases" rather than "granule-bound starch synthases".

EXAMPLE 10

10 **Analysis of wheat starch synthase II mRNA expression**

The mRNA for wheat starch synthase II could be detected in leaves, pre-anthesis florets and endosperm of wheat when total RNAs isolated from these tissue were probed with a PCR probe, wSSIIP2, corresponding to nucleotide positions 1435 to 1835 bp of wSSIIB-cDNA (SEQ ID NO:1; Figure 4). Unlike wSSI, which could not be detected in wheat leaves derived from plants grown under the same conditions, wSSII genes are highly-expressed in the leaves (Figure 4, lane 1), and expressed at an intermediate level in pre-anthesis florets (Figure 4, lane 2), and at much lower levels in developing wheat endosperm cells (Figure 4, lanes 3-11). In contrast, the maize SSIIa is expressed predominantly in the endosperm, whilst the maize SSIIb is detected mainly in the leaf, albeit at low levels (Harn *et al.*, 1998).

The wSSII mRNA was detectable in the endosperm 6 days after anthesis and mRNA levels increase between 8 and 18 days post-anthesis, after which time levels of mRNA decline.

Southern blotting experiments in wheat demonstrated that the wSSIIP2 probe used detected only a single copy of the SSII gene in each genome (data not shown). Thus, it is unlikely that this probe cross-hybridised with mRNAs encoded by genes other than wSSII.

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EXAMPLE 11

Chromosomal localization of the wheat wSSII genes.

I. Amplification of specific cDNA regions of wheat starch synthase II using PCR

Two PCR products, wSSIIp2 and wSSIIp3 were amplified from the cDNA clone wSSIIb
5 and used for the northern hybridisation and Southern hybridisation, respectively.

The primers sslIa (5' TGTGAGGTTCATGGCACGTTC 3': SEQ ID NO: 25) and sslIb
(5' AGTCGTTCTGCCGTATGATGTCG 3': SEQ ID NO: 26) were used to amplify the
cDNA fragment wSSIIp2 (i.e. nucleotide positions 1435 to 1835 of SEQ ID NO:1).

10

The primers sslIc (5' CCAAGTACCAGTGGTGAACGC 3': SEQ ID NO: 27) and sslId
(5' CGGTGGGATCCAACGGCCC 3': SEQ ID NO: 28) were used to amplify the cDNA
fragment wSSIIp3 (i.e. nucleotide positions 2556 to 2921 of SEQ ID NO:1).

15 The amplification reactions were performed using a FTS-1 thermal sequencer (Corbett,
Australia) for 1 cycle of 95°C for 2 minutes; 35 cycles of 95°C for 30 seconds, 60°C for
1 minutes, 72°C for 2 minutes and 1 cycle of 25°C for 1 minute.

II. PCR and nucleotide sequence analysis of 3' sequences of wheat SSII genes

20 Genomic DNA was extracted from wild-type Chinese Spring wheat, and from three
nullisomic-tetrasomic lines of chromosome 7 of Chinese Spring wheat, and from
Triticum tauschii (var strangulata, accession number CPI 100799), and used as a
template for the amplification and nucleotide sequence analysis of wheat SSII genes.

25 RFLP analysis of *Bam*HI and *Eco*RI restricted DNA from each wheat or *T. Tauschii* line
was carried out using the wSSIIp3 fragment as a probe. Three hybridising bands were
obtained which could be assigned to chromosomes 7A, 7B and 7D, respectively (data
not shown). This analysis indicates that there is a single copy of the wSSII gene in
each genome in hexaploid wheat, consistent with the findings of Yamamori and Endo
30 (1996) who located the SGP-A1, B1 and D1 proteins to the short arm of chromosome
7.

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PCR analysis was used to assign each of the cDNA clones to the individual wheat genomes. A single 365 bp PCR fragment was obtained from nullisomic-tetrasomic genomic DNA of Chinese Spring when primers *sslIc* and *sslId* were used for the PCR amplification (Figure 5, right panel). This PCR product is obtained only from lines
5 bearing the B genome. The fragment was cloned and sequenced and shown to be identical to a 365 bp region of the *wSSIIB* cDNA. An identical fragment is obtained by PCR amplification of the *wSSIIB* cDNA clone, but not by amplification of the *wSSIIA* or *wSSIID* clones, supporting the conclusion that the *wSSIIB* cDNA is the product of a gene located on chromosome 7 of the B genome of hexaploid wheat.

10

Two PCR products were also amplified from nullisomic-tetrasomic genomic DNA of Chinese Spring using the primers *sslIc* and *sslIe* (Figure 5, left panel). One PCR fragment, approximately 350 bp is only amplified when the A genome is present, and a second 322 bp product is only amplified when the D-genome is present. The 350 and
15 322 bp PCR products were also cloned and sequenced and shown to be identical to the *wSSIIA* and *wSSIID* cDNAs, respectively, supporting the conclusion that the *wSSIIA* and *wSSIID* cDNAs are the products of genes located on chromosomes 7A and 7D, respectively.

20

EXAMPLE 12

Isolation of genomic *wSSII* clones

Screening of a genomic library from the D-genome donor of wheat, *T. tauschii*, was performed as described in Example 5, using the PCR-derived DNA fragment *wSSIIP2* as a hybridisation probe. A positive-hybridising clone, designated *wSSII-8*, and
25 comprising a putative *T. tauschii* homologue of the *wSSII* gene, was isolated.

Positive-hybridising plaques were digested using the restriction enzyme *Bam*HI, separated on a 1% agarose gel, transferred to nitrocellulose membrane and hybridised to probe *wSSIIP4* comprising nucleotides 1 to 367 of the *wSSIIA* cDNA clone, using
30 the conditions described by Rahman *et al.* (1997). Clone *wSSII-8* also hybridises strongly to the *wSSIIP4* probe, confirming its identity as a genomic *wSSII* gene.

The complete nucleotide sequence of the wSSII gene was determined and is presented herein as SEQ ID NO: 37. The structural features of this gene are present in Table 3. A schematic representation of the intron/exon organisation of this gene is also presented in Figure 6.

5

TABLE 3**Structural features of the wheat starch synthase II genomic gene**

| | Nucleotide Position in SEQ ID NO: 37 | Feature | Length (bases) |
|----|---|--|-----------------------|
| 10 | 1- 1416 | 5'-untranscribed region and promoter sequence | 1416 |
| | 1417 - 1743 | exon 1 | 327 |
| | 1480-1482 | translation start codon (ATG) | 3 |
| | 1744 - 1847 | intron 1 | 104 |
| | 1848 - 2553 | exon 2 | 706 |
| 15 | 2554 - 2641 | intron 2 | 88 |
| | 2642 - 2706 | exon 3 | 65 |
| | 2707 - 3606 | intron 3 | 900 |
| | 3607 - 3684 | exon 4 | 78 |
| | 3685 - 3773 | intron 4 | 89 |
| 20 | 3774 - 3884 | exon 5 | 111 |
| | 3885 - 3981 | intron 5 | 97 |
| | 3982 - 4026 | exon 6 | 45 |
| | 4027 - 4406 | intron 6 | 380 |
| | 4407 - 4580 | exon 7 | 174 |
| 25 | 4581 - 7296 | intron 7 | 2716 |
| | 7297 - 8547 | exon 8 | 1251 |
| | 8251 - 8253 | translation stop codon (TGA) | 3 |
| | 8548 -9024 | 3'-untranscribed region | 477 |

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EXAMPLE 13

Cloning of specific cDNA regions of wheat starch synthase III using RT-PCR
PCR primers were used to amplify sequences of starch synthase III from wheat endosperm cDNA. The design of PCR primers was based on the sequences of starch
5 synthase III from potato and the *du1* starch synthase III gene of maize.

First-strand cDNAs were synthesised from 1 μ g of total RNA (derived from endosperm of the cultivar Rosella, 12 days after anthesis) as described by Maniatis *et al.* (1982), and then used as templates to amplify two specific cDNA regions, wSSIIIp1 and
10 wSSIIIp2, of wheat starch synthase III by PCR.

The primers used to obtain the cDNA clone wSSIIIp1 were as follows:
Primer wSS3pa (5' GGAGGTCTTGGTGATGTTGT 3': SEQ ID NO: 29); and
Primer wSS3pb (5' CTTGACCAATCATGGCAATG 3': SEQ ID NO: 30).

15

The primers used to obtain the cDNA clone wSSIIIp2 were as follows:
Primer wSS3pc (5' CATTGCCATGATTGGTCAAG 3': SEQ ID NO: 31); and
Primer wSS3pd (5' ACCACCTGTCCGTTCCGTTGC 3': SEQ ID NO: 32).

20 The amplified clones wSSIIIp1 and wSSIIIp2 were used as probes to screen the third cDNA library and *T. tauschii* genomic DNA library as described in Example 4.

A further probe designated wSSIIIp3 was used for screening the third cDNA library, as described in Example 4. Probe wSSIIIp3 was amplified by PCR from a cDNA clone
25 produced from the first screening using the following amplification primers:
Primer wSS3pe (5' GCACGGTCTATGAGAACAATGGC 3': SEQ ID NO: 33); and
Primer wSS3pf (5' TCTGCATACCACCAATCGCCG 3': SEQ ID NO: 34).

The amplification reactions were performed using a FTS-1 or FTS4000 thermal
30 sequencer (Corbett, Australia) for 1 cycle of 95°C for 2 minutes; 35 cycles of 95°C for 30 seconds, 60°C for 1 minutes, 72°C for 2 minutes and 1 cycle of 25°C for 1 minute.

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Amplified sequences of the expected length were obtained, cloned and sequenced, and shown to contain DNA sequences highly homologous to the maize and potato SSIII genes. PCR fragments were subsequently used to probe a wheat cDNA library
5 by DNA hybridisation and 8 positive clones were obtained, including one 3 kb cDNA. A region from the 5' end of this cDNA was amplified by PCR and used a probe for a second round of screening the cDNA library, obtaining 8 cDNA clones. Of these, one cDNA was demonstrated to be full length (wSSIII.B3, 5.36 kb insert). The sequence of the 5,346 bp wSSIII.B3 cDNA clone is given in SEQ ID NO:7.

10

Sequencing of the 8 cDNA clones obtained from the second round screening of the wheat cDNA library revealed that there were at least 2 classes of cDNA encoding SSIII present, possibly being encoded by homeologous genes on different wheat genomes. The sequence of a representative of this second class of cDNA clones, wSSIII.B1, is
15 shown in SEQ ID NO:9. The 3261 bp clone wSSIII.B1 is not full length, however it is similar to nucleotides 1739 to 5346 of the homeologous clone wSSIII.B3 (SEQ ID NO: 7). Clone wSSIII.B1 has an open reading frame between nucleotide positions 1 and 3177.

20 An open reading frame is found in the cDNA clone wSSIII.B3 (SEQ ID NO:7), in the region between position 29, commencing the ATG start codon, and nucleotide position 4912. The amino acid sequence deduced from this open reading frame is shown in SEQ ID NO:8.

25 An alignment of the deduced amino acid sequences of SSIII from maize, potato and wheat is shown in Figure 7. There is about 56.6% identity between the maize SSIII and wheat wSSIII.B3 sequence at the amino acid level.

The C-terminal domain of starch synthases comprise the catalytic domain, and a
30 characteristic amino acid sequence motif KVGGLGDVVTSLSRVQDLGHNVEV (SEQ ID NO: 35) in maize, or alternatively KVGGLGDVVTSLSRAIQDLGHTVEV (SEQ ID

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NO: 36) in wheat, marking the first conserved region in the C-terminal domain. This amino acid sequence is present at amino acid residues 1194 to 1218 of SEQ ID NO: 8.

5 The amino acid identity between maize dull1 and wSSIII.B3 in the N-terminal region (i.e. amino acids 1 to 600 in Figure 7) is only 32.2%; whilst the amino acid identity in the central region (i.e. amino acids 601 to 1248 in Figure 7) is 68.4%; and in the C-terminal region (i.e. amino acids 1249 to 1631 in Figure 7) is 84.6%. Accordingly, the SSIII starch synthases are much more highly conserved between maize and wheat in
10 the region comprising the catalytic domain of the proteins.

EXAMPLE 14

Analysis of wheat starch synthase III mRNA expression

Figure 8 shows the expression of wSSIII mRNA during endosperm development in two
15 wheat varieties grown under defined environmental conditions. The expression of the gene is seen very early in endosperm development in both cultivars, 4 days after anthesis (Figure 8, panels a and b). Expression in the leaf of the variety Gabo is very weak (Figure 8, panel c, Lane L) whereas strong expression is seen in pre-anthesis florets (Figure 8, panel c, Lane P).

20

EXAMPLE 15

Amino acid sequence comparisons between wheat SSII and SSIII polypeptides

Amino acid sequence comparisons between wheat BSSS, SSI, SSII and SSIII
25 polypeptides reveals eight highly-conserved domains (Figure 9). The amino acid sequences of these domains are represented in the wheat SSIII amino acid sequence by the following sequence motifs:

- (a) Region 1: KVGGLGDVVT;
- (b) Region 2: GHTVEVILPKY;
- 30 (c) Region 3: HDWSSAPVAWLYKEHY;
- (d) Region 4: GILNGIDPDIWDPYTD;

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- (e) Region 5: DVPIVGIITRLTAQKG;
- (f) Region 5a: NGQVVLLGSA;
- (g) Region 6: AGSDFIIVPSIFEPGLTQLVAMRYGS; and
- (h) Region 7: TGGLVDTV.

5

These conserved amino acid sequences are summarised in Table 4. As shown in Table 4 below, there is at least about 25% amino acid sequence identity, preferably at least about 30% amino acid sequence identity, more preferably at least about 35% amino acid sequence identity, more preferably at least about 40% amino acid sequence identity, more preferably at least about 45% amino acid sequence identity, more preferably at least about 50% amino acid sequence identity, more preferably at least about 55% amino acid sequence identity, more preferably at least about 60% amino acid sequence identity, more preferably at least about 65% amino acid sequence identity, more preferably at least about 70% amino acid sequence identity, more preferably at least about 75% amino acid sequence identity, more preferably at least about 80% amino acid sequence identity, more preferably at least about 85% amino acid sequence identity, more preferably at least about 90% amino acid sequence identity and even more preferably at least about 95% amino acid sequence identity between the amino acid sequences of plant starch synthase enzymes, in particular wheat starch synthases.

From the data presented in Table 4, the most conserved regions of the wheat SSII and SSIII polypeptides are a region of 6 or 7 identical amino acids in Region 1 and a region of 8 or 9 identical amino acids in Region 6. The lowest regions of identity are found in regions 3 and 5a.

For each of the amino acid sequences presented in the first column of Table 4, which are specific for wSSIII polypeptides, corresponding signature motifs which are specific for wSSII-A, wSSII-B, and wSSII-D polypeptides can be derived from the alignment, as follows:

Region 1: KTGGLGDVAGA;

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- Region 2: GHRVMVVVPRY;
Region 3: NDWHTALLPVYLKAYY;
Region 4: GIVNGIDNMEWNPEVD;
Region 5: DVPLLGFGRLDGQKG;
5 Region 5a: DVQLVMLGTG;
Region 6: AGADALLMPSRF(E/V)PCGLNQLYAMAYGT; and
Region 7: VGG(V/L)RDTV.

Comparison of the amino acid sequences of all available starch synthases with the
10 deduced amino acid sequences of the three wSSII cDNA clones of the present
invention (i.e. wSSIIB, wSSIIA and wSSIID) was conducted using PILEUP analysis
(Devereaux *et al.*, 1984) and data are presented herein as a dendrogram (Figure 10).
The sequence of the glycogen synthase of *E. coli* was also included. Based upon their
amino acid similarities, four classes of plant starch synthases can be defined: GBSS,
15 SSI, SSII and SSIII.

Table 5 shows that levels of identity at the amino acid level between the wSSII
sequences, as determined using the BESTFIT programme in GCG (Devereaux *et al.*,
1984), and other class II starch synthases range from 70% identity with potato SSII to
20 85% identity with maize SSIIa. Both wSSIIB and wSSIID showed significantly higher
homology to maize SSIIa than wSSIIA. Based upon sequence identities and the
function of the Sgp-1 proteins in wheat, the wSSIIB, wSSIIA and wSSIID cDNA clones
are members of the starch synthase II (SSII) group and are more similar in sequence
to maize SSIIa than maize SSIIb.

25

TABLE 4**Identities between conserved motifs of plant starch synthases**

| | Sequence in wSSIII polypeptide | Number of conserved residues between wheat starch synthases | Number of conserved residues between wheat SSII and SSIII polypeptides |
|----|---|--|---|
| 5 | Region 1: KVGGLGDVVT | 6/11 residues | 6/11 residues |
| | Region 2: GHTVEVILPKY | 6/11 residues | 6/11 residues |
| 10 | Region 3: HDWSSAPVAWLYKEHY | 4/16 residues | 5/16 residues |
| | Region 4: GILNGIDPDIWDPYTD | 7/16 residues | 8/16 residues |
| | Region 5: DVPIVGIIITRLTAQKG | 8/16 residues | 10/16 residues |
| 15 | Region 5a: NGQVVLLGSA | 4/10 residues | 4/10 residues |
| | Region 6: AGSDFIIVPSIFPCGLT QLVAMRYGS | 15/27 residues | 17/27 residues |
| 20 | Region 7: TGGLVDTV | 5/9 residues | 5/9 residues |

TABLE 5

| | wSSII-A | wSSII-B | wSSII-D |
|----------------|---------|---------|---------|
| wSSI-A | 100% | | |
| wSSII-B | 95.9% | 100% | |
| 5 wSSII-D | 96.3% | 96.7% | 100% |
| maize SSIIa | 76.1% | 85.2% | 84.7% |
| maize SSIIb | 76.3% | 76.7% | 75.9% |
| pea SSII | 72.0% | 72.2% | 71.8% |
| 10 potato SSII | 70.9% | 71.1% | 70.3% |

Figure 11 shows a schematic representation of an alignment of plant starch synthase sequences, including wheat GBSS, wheat SSI, wheat SSII-A1, maize SSIIa, and maize dull-1 polypeptides, in which the position of the first homologous region, comprising the consensus motif KXGG, is used as the basis of the alignment. The major differences in structure between the classes of genes are found in the length of the N-terminal region between the transit peptide and the first conserved region. At one extreme, the GBSS genes have a very short N-terminal arm, whereas the *du1* starch synthase contains a very long N-terminal extension containing several distinct regions. The wSSII genes contain an N-terminal extension which is longer than either GBSS, SSI, or SSIIb, and slightly longer than the maize SSIIa gene.

EXAMPLE 16

Isolation of genomic clones for SSIII

Screening of a genomic library from the D-genome donor of wheat, *T. tauschii*, identified a number of clones which hybridised to the wSSIII PCR fragment. Positive plaques in the genomic library were selected as those hybridising with a probe that had been generated by PCR (amplifying between nucleotide positions 3620 to 3966) from the SSIII cDNA as template. The primer sequences used were as follows:

wSS3pa (5' GGAGGTCTTGGTGATGTTGT 3': SEQ ID NO: 29); and
 30 wSS3pb (5' CTTGACCAATCATGGCAATG 3' : SEQ ID NO: 30).

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Hybridisation was carried out in 25% formamide, 6 x SSC, 0.1% SDS at 42 °C for 16 hour, then washed three times with 2 x SSC containing 0.1% SDS at 65 °C, for 1 hour per wash. shows an example of a plaque lift showing positive and negative hybridisations for plaques containing the *T. tauschii* homologue of the wSSIII.B3 gene.

5

DNA was isolated from positive-hybridising λ clones using methods described by Maniatis *et al.* Briefly, DNA was digested using *Bam*HI or *Bgl*II and sub-cloned in to the vector pJKKmfm. DNA sequencing was performed using the automated ABI system with dye terminators as described by the manufacturers. DNA sequences were
10 analysed using the GCG suite of programs (Devereaux *et al.*, 1984).

Nucleotide sequences of the genomic SSIII clone from *T. tauschii* are provided herein as 6 contiguous sequences designated fragments 1 to 6 (SEQ ID NOs: 11 to 16, respectively). Table 6 defines the relative positions of these fragments with respect to
15 the SSIII cDNA and describes the positions of exons. Figure 11 shows this information schematically.

The complete nucleotide sequence of a wheat SSIII genomic gene is presented herein as SEQ ID NO: 38. The structural features of this gene are presented in Table 7. A
20 schematic representation of the intron/exon organisation of this gene is also presented in Figure 12.

EXAMPLE 17

Discussion

25 Early work on the Sgp-1 starch synthase proteins (Denyer *et al.*, 1995; Rahman *et al.*, 1995) was based on the localisation of these proteins in the wheat starch granule, and no definitive conclusion concerning their presence or absence in soluble extracts of the wheat endosperm was presented.

30 We have now demonstrated that a monoclonal antibody against the Sgp-1 proteins cross reacts strongly with those starch synthase proteins having apparent molecular

The present invention provides cDNA and genomic clones encoding the wSSII and wSSIII polypeptides and the corresponding genomic clones. Whilst the evidence is compelling that the wSSIIA, wSSIIB and wSSIID cDNAs encode the Sgp-A1, Sgp-B1 and Sgp-D1 proteins of the wheat starch granule, molecular weights calculated from the deduced amino acid sequences of the clones are considerably lower than estimates obtained from SDS-PAGE. The molecular weight of the precursor wSSIIA protein is 87,229 Da, and the mature protein 81,164 Da, yet the estimated molecular weight in our experience is 105 kDa. The assignment of the wSSIIA cDNA to the A-genome of wheat is demonstrated in Figure 5, and the assignment of the 105 kDa protein to the A-genome in Denyer *et al.* (1995) and Yamamori and Endo (1996). Similarly, the molecular weight of the wSSIIB protein is 86,790 Da and the mature protein 80,759 Da, yet the molecular weight of the Sgp-B1 protein is estimated to be 100 kDa. No comparison can be made of the wSSIID sequences as a full length cDNA clone was not obtained. The wSSIIA and wSSIIB amino acid sequences differ by just a single amino acid residue, yet there is an apparent difference of 5 kDa in molecular weight when estimated by SDS-PAGE. Several possibilities can be advanced to account for this apparent discrepancy in molecular weights. Firstly, the wSSII proteins may not migrate in SDS-PAGE in accordance with their molecular weight because they

retain some conformation under the denaturing conditions used. Secondly, the proteins may be glycosylated. It is also possible that the proteins may be non-covalently linked to starch through a high affinity starch binding site which survives denaturation and SDS-PAGE. Differences between the apparent molecular weights and those calculated from the deduced amino acid sequences will have to be defined in establishing the relationship between the wSSII proteins and proteins encoded by the analogous SSII genes of other species.

The catalytic domain of the starch synthases is found at the C-terminal end of the protein (Gao *et al.*, 1998; Harn *et al.*, 1998). Harn *et al.* (1998) identified 7 conserved regions among SSIIa, SSIIb, SSII and GBSS sequences. We have identified an additional conserved region (designated region 5a in Table 4 and Figure 10) comprising the amino acid sequence motif DVQLVMLGTG, by a comparison of the wSSII and wSSIII sequences of the present invention with differing isoforms of other plant starch synthases (GBSS, SSII, SSII and SSIII). The conservation of eight peptide regions among the 4 classes of starch synthases is striking, in terms of their sequence homologies and their alignment.

Analysis of the wheat SSII genes shows that there is a motif, PVNGENK, which is repeated. The area surrounding the repeated PVNGENK motif is not homologous to maize SSIIa and the insertion of this region is responsible for the difference in length between the wheat SSII and maize SSIIa genes. In pea and potato SSII polypeptides, a PPP motif (Figure 3; residues 251-253 and 287-289 respectively) has been suggested to mark the end of the N-terminal region and to facilitate the flexibility of an "N-terminal arm". This motif is not found in either the maize or wheat SSII sequences.

The generation of a wheat line combining null alleles at each of the three wSSII loci, wSSIIA, wSSIIB and wSSIID, has been reported recently by Yamamori (1998). In this triple null line, the large starch granules were reported to be mostly deformed and a novel starch with high blue value was observed when stained with iodine, indicating that wSSII is a key enzyme for the synthesis of starch in wheat. Further analysis of the

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starch derived from this triple null mutant is in progress.

Mutations in starch synthases are known in three other species. In pea, mutation in SSII gives rise to starch with altered granule morphology and an amylopectin which yields an oligosaccharide distribution with reduced chain length on debranching, compared to the wild type (Craig *et al.*, 1998). A similar mutation in a gene designated SSII is known in *Chlamydomonas* (the *sta-3* mutation) and similar effects on granule morphology and amylopectin structure are observed (Fontaine *et al.*, 1993). In maize, two mutations affecting starch synthases are known. First, the *dull1* mutation has been shown to be caused by a lesion within the *du1* SSIII-type starch synthase gene (Gao *et al.*, 1998). A second mutation, the *sugary-2* mutation yields a starch with reduced amylopectin chain lengths on debranching (this mutation co-segregates with the SSIIa locus (Harn *et al.*, 1998) although direct evidence that the *sugary-2* mutation is caused by a lesion in the SSIIa gene is lacking). In the SSII mutants of each of these species, amylose biosynthesis capacity is retained, suggesting different roles in amylose and amylopectin synthesis for the GBSS and SSII genes. Given the conservation in overall organisation of the GBSS and SSII genes (see Figures 12 and 13), when an alignment is made based on the KTGGL motif of the first conserved region, this focuses attention on the role(s) of the N-terminal region in defining substrate specificity and the localisation of the proteins as the N-terminal region is the major area of divergence between the 4 classes of starch synthases. However, it is premature to exclude the influence of more subtle mutations in central and C-terminal regions of the gene.

The cloning of the wSSII and wSSIII cDNAs and genomic clones described herein provides useful tools for the further study of the roles of the starch synthases in wheat. Firstly, they provide a source of markers which can be used to recover and combine null or divergent alleles. Secondly, genetic manipulation of wheat by gene suppression or over-expression can be carried out, and the genes may be used for over expression in other species. The promoter regions of these genes are also useful in regulating the expression of starch synthase genes and other heterologous genes in the developing wheat endosperm and in pre-anthesis florets of wheat.

TABLE 6
Summary of the Wheat Starch Synthase III Genomic Sequence

| Fragment in genomic DNA clone | Length (bp) | Features in SEQ ID NOS:11 to 16 | Corresponding region in cDNA sequence |
|-------------------------------|-------------|--|--|
| Fragment 1 (SEQ ID NO: 11) | 728 | Translation start codon (nucleotides 287 to 289); Exon 1.1 (nucleotides 260 to 385). | Exon 1.1: nucleotides 1 to 126 |
| Fragment 2 (SEQ ID NO: 12) | 2446 | Exon 2.1 (nucleotides 1 to 1938); Exon 2.2 (nucleotides 2197 to 2418). | Exon 2.1: nucleotides 1008 to 2948; Exon 2.2: nucleotides 2949 to 3171 |
| Fragment 3 (SEQ ID NO: 13) | 1032 | Exon 3.1 (nucleotides 310 to 580) | Exon 3.1: nucleotides 3172 to 3440 |
| Fragment 4 (SEQ ID NO: 14) | 892 | Exon 4.1 (nucleotides 678 to 853) | Exon 4.1: nucleotides 3441 to 3616 |
| Fragment 5 (SEQ ID NO: 15) | 871 | Partial Exon 5.1 (nucleotides 1 to 29) Exon 5.2 (nucleotides 293 to 463) Exon 5.3 (nucleotides 589 to 695) | Exon 5.1: nucleotides 3908 to 3937 (partial) Exon 5.2: nucleotides 3938 to 4108 Exon 5.3: nucleotides 4109 to 4215 |
| Fragment 6 (SEQ ID NO: 16) | 1583 | Exon 6.1 (nucleotides 471 to 653); Exon 6.2 (nucleotides 770 to 902); Exon 6.3 (nucleotides 999 to 1110); Exon 6.4 (nucleotides 1201 to 1328); Partial Exon 6.5 (nucleotides 1408 to 1583); Translation stop codon (nucleotides 1536 to 1538) | Exon 6.1: nucleotides 4238 to 4420 Exon 6.2: nucleotides 4421 to 4552 Exon 6.3: nucleotides 4553 to 4664 Exon 6.4: nucleotides 4665 to 4793 Exon 6.5: nucleotides 4794 to 4966 (partial) |

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

| | Nucleotide Position in SEQ ID NO: 38 | Feature | Length (bases) |
|----|---|---|----------------|
| 5 | 1- 973 | 5'-untranscribed region and promoter sequence | 973 |
| | 974 - 1099 | exon 1 | 126 |
| | 1001-1003 | translation start codon (ATG) | 3 |
| | 1100 - 2056 | intron 1 | 957 |
| | 2057 - 2120 | exon 2 | 64 |
| 10 | 2121 - 2588 | intron 2 | 468 |
| | 2589 - 5291 | exon 3 | 2703 |
| | 5292 - 5549 | intron 3 | 258 |
| | 5550 - 5767 | exon 4 | 218 |
| | 5768 - 6103 | intron 4 | 336 |
| 15 | 6104 - 6374 | exon 5 | 271 |
| | 6375 - 7148 | intron 5 | 774 |
| | 7149 - 7324 | exon 6 | 176 |
| | 7325 - 7438 | intron 6 | 114 |
| | 7439 - 7546 | exon 7 | 108 |
| 20 | 7547 - 7792 | intron 7 | 246 |
| | 7793 - 7902 | exon 8 | 110 |
| | 7903 - 8797 | intron 8 | 895 |
| | 8798 - 8900 | exon 9 | 103 |
| | 8901 - 9164 | intron 9 | 264 |
| 25 | 9165 - 9335 | exon 10 | 171 |
| | 9336 - 9460 | intron 10 | 125 |
| | 9461 - 9589 | exon 11 | 129 |
| | 9590 - 9677 | intron 11 | 88 |

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| | | | |
|----|---------------|------------------------------|-----|
| | 9678 - 9860 | exon 12 | 183 |
| | 9861 - 9977 | intron 12 | 117 |
| | 9978 - 10109 | exon 13 | 132 |
| | 10110 - 10205 | intron 13 | 96 |
| 5 | 10206 - 10317 | exon 14 | 112 |
| | 10318 - 10407 | intron 14 | 90 |
| | 10408 - 10536 | exon 15 | 129 |
| | 10537 - 10618 | intron 15 | 82 |
| | 10619 - 11146 | exon 16 | 128 |
| 10 | 10744 - 10746 | translation stop codon (TGA) | 3 |
| | 11147 - 11611 | 3'-untranscribed region | 465 |

REFERENCES

- 15 1. Ausubel, F. M., Brent, R., Kingston, RE, Moore, D.D., Seidman, J.G., Smith, J.A., and Struhl, K. (1987). *In: Current Protocols in Molecular Biology*. Wiley Interscience (ISBN 047150338).
2. Abel GJW, Springer F, Willmitzer L, Kossmann J (1996) Cloning and functional analysis of a cDNA encoding a novel 139 kDa starch synthase from potato (*Solanum*
20 *tuberosum* L.). *Plant J* **10**: 981-991.
3. Ainsworth C, Clark J, Balsdon J (1993) Expression, organisation and structure of the genes encoding the waxy protein (granule-bound starch synthase) in wheat. *Plant Mol Biol* **22**: 67-82.
4. Baba T, Nishihara M, Mizuno K, Kawasaki T, Shimada H, Kobayabashi E,
25 Ohnishi S, Tanaka K, Arai Y (1993) Identification, cDNA cloning, and Gene Expression of Soluble Starch Synthase in Rice (*Oryza sativa* L.) Immature Seeds. *Plant Physiol* **103**: 565-573.
5. Craig J, Lloyd JR, Tomlinson K, Barber L, Edwards A, Wang TL, Martin C, Hedley CL, Smith AM (1998) Mutations in the gene encoding starch synthase II
30 profoundly alter amylopectin structure in pea embryos. *Plant Cell* **10**: 413-426.

6. Denyer K, Hylton CM, Jenner CF, Smith AM (1995) Identification of multiple isoforms of soluble and granule-bound starch synthase in developing wheat endosperm. *Planta* **196**: 256-265.
7. Devereaux, J, Haeberli P, Smithies O (1984) A comprehensive set of sequence analysis programs for the VAX. *Nucleic Acids Res* **12**: 387-395.
8. Dry I, Smith A, Edwards A, Bhattacharyya M, Dunn P, Martin C (1992) Characterisation of cDNAs encoding two isoforms of granule-bound starch synthase which show differential expression in developing storage organ of pea and potato. *Plant J* **2**: 193-202.
- 10 9. Edwards A, Marshall J, Sidebottom C, Visser RGF, Smith AM, Martin C (1995) Biochemical and molecular characterization of a novel starch synthase from potato tubers. *Plant J* **8**: 283-294.
10. Fontaine T, D'Hulst C, Maddelein M-L, Routier F, Pépin TM, Decq A, Wieruszeski J-M, Delrue B, Van den Koornhuyse N, Bossu J-P, Fournet B, Ball S
15 (1993) Toward an understanding of the biogenesis of the starch granule. Evidence that *Chlamydomonas* soluble starch synthase II controls the synthesis of intermediate size glucans of amylopectin. *J Biol Chem* **22**: 16223-16230.
11. Furukawa K, Tagaya M, Inouye M, Preiss J, Fukui T (1990) Identification of lysine 15 at the active site in *Escherichia coli* glycogen synthase. *J Biol Chem* **265**:
20 2086-2090.
12. Gao M, Wanat J, Stinard PS, James MG, Myers AM (1998) Characterization of dull1, a maize gene coding for a novel starch synthase. *Plant Cell* **10**: 399-412.
13. Harn C, Knight M, Ramakrishnan A, Guan H, Keeling PL, Wasserman BP (1998) Isolation and characterization of the zSSIIa and zSSIIb starch synthase cDNA
25 clones from maize endosperm. *Plant Mol Biol* **37**: 639-649.
14. Kloesgen RB, Gierl A, Schwarz-Sommer ZS, Saedler H (1986) Molecular analysis of the waxy locus of *Zea mays*. *Mol Gen Genet* **203**: 237-244.
15. Knight ME, Harn C, Lilley CER, Guan H, Singletary G W, MuForster C, Wasserman BP, Keeling PL (1998) Molecular cloning of starch synthase I from maize
30 (W64) endosperm and expression in *Escherichia*. *Plant J* **14**: 613-622.
16. Kumar A, Larsen CE, Preiss J (1986) Biosynthesis of bacterial glycogen:

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- Primary structure of *Escherichia coli* ADP-glucose:alpha-1,4-glucan, 4-glucosyltransferase as deduced from the nucleotide sequence of the *glgA* gene. J Biol Chem **261**: 16256-16259.
17. Li Z, Rahman S, Kosar-Hashemi B, Mouille G, Appels R Morell, MK (1999)
5 Cloning and characterisation of a gene encoding wheat starch synthase I. Theor Appl Genet: *In press*.
18. Mouille G, Maddelein M-L, Libessart N, Talaga P, Decq A, Delrue B Ball, S (1996). Preamylopectin processing: A mandatory step for starch biosynthesis in plants. Plant Cell **8**: 1353-1366.
- 10 19. Nakamura T, Yamamori M, Hirano H, Hidaka S, Nagamine T (1995) Production of waxy (amylose-free) wheats. Mol Gen Genet **248**: 253-259.
20. Okagaki, RJ (1992) Nucleotide sequence of a long cDNA from the rice waxy gene. Plant Mol Biol **19**: 513-516.
21. Ozbun, J.L., Hawker, J.S. and Preiss, J. (1971) Adensine diphosphoglucose-
15 starch glucosyltransferases from developing kernels of waxy maize. Plant Physiology **48**: 765-769
22. Ozbun, J.L., Hawker, J.S., Greenberg, E., Lammel, C., Preiss, J. and Lee, E.Y.C.(1973) Starch synthetase, phosphorylase, ADPglucose pyrophosphorylase, and UDPglucose pyrophosphorylase in developing maize kernels. Plant Physiology **51**: 1-
20 5.
23. Pollock, C. and Preiss, J.(1980) The citrate-stimulated starch synthase of starchy maize kernels: purification and properties. Arch Biochem Biophys **204**: 578-588.
24. Rahman S, Abrahams S, Abbott D, Mukai Y, Samuel M, Morell M, Appels R
25 (1997) A complex arrangement of genes at a starch branching enzyme I locus in D-genome donor of wheat. Genome **40**: 465-474.
25. Rahman S, Kosar-Hashemi B, Samuel M, Hill A, Abbott DC, Skerritt JH, Preiss J, Appels R, Morell M (1995) The major proteins of wheat endosperm starch granules. Aust J Plant Physiol **22**: 793-803.

26. Rahman S, Li Z, Abrahams S, Abbott D, Appels R, Morell M (1998) Characterisation of a gene encoding wheat endosperm starch branching enzyme-I. *Theor Appl Genet* **98**: *In press*.
27. Sears ER, Miller TG (1985) The history of Chinese spring wheat. *Cereal Res Comm* **13**: 261-263.
28. Takaoka M, Watanabe S, Sassa H, Yamamori M, Nakamura T, Sasakuma T, Hirano H (1997) Structural characterisation of high molecular weight starch granule-bound proteins in wheat (*Triticum aestivum* L). *J Agric Food Chem* **45**: 2929-2934.
29. van der Leij FR, Visser RGF, Ponstein AS, Jacobsen E, Feenstra WJ (1991) Sequence of the structural gene for granule bound starch synthase of potato (*Solanum tuberosum* L.) and evidence for a single point deletion in the *amf* allele. *Mol Gen Genet* **228**: 240-248.
30. Yamamori M, Endo TR (1996) Variation of starch granule proteins and chromosome mapping of their coding genes in common wheat. *Theor Appl Genet* **93**: 275-281.
31. Yamamori M (1998) Selection of a wheat lacking a putative enzyme for starch synthesis, SGP-1 *Proc 9th In Wheat Gen Symp* **4**, 300-302.

CLAIMS:

1. An isolated nucleic acid molecule which comprises a sequence of nucleotides selected from the group consisting of:
 - (i) the nucleotide sequence set forth in SEQ ID NO: 1 or the protein-encoding region thereof or a degenerate nucleotide sequence thereto;
 - (ii) the nucleotide sequence set forth in SEQ ID NO: 3 or the protein-encoding region thereof or a degenerate nucleotide sequence thereto;
 - (iii) the nucleotide sequence set forth in SEQ ID NO: 5 or the protein-encoding region thereof or a degenerate nucleotide sequence thereto;
 - (iv) the nucleotide sequence set forth in SEQ ID NO: 7 or the protein-encoding region thereof or a degenerate nucleotide sequence thereto;
 - (v) the nucleotide sequence set forth in SEQ ID NO: 9 or the protein-encoding region thereof or a degenerate nucleotide sequence thereto;
 - (vi) the nucleotide sequence set forth in SEQ ID NO: 11 or the protein-encoding region thereof or a degenerate nucleotide sequence thereto;
 - (vii) the nucleotide sequence set forth in SEQ ID NO: 12 or the protein-encoding region thereof or a degenerate nucleotide sequence thereto;
 - (viii) the nucleotide sequence set forth in SEQ ID NO: 13 or the protein-encoding region thereof or a degenerate nucleotide sequence thereto;
 - (ix) the nucleotide sequence set forth in SEQ ID NO: 14 or the protein-encoding region thereof or a degenerate nucleotide sequence thereto;
 - (x) the nucleotide sequence set forth in SEQ ID NO: 15 or the protein-encoding region thereof or a degenerate nucleotide sequence thereto;
 - (xi) the nucleotide sequence set forth in SEQ ID NO: 16 or the protein-encoding region thereof or a degenerate nucleotide sequence thereto;
 - (xii) the nucleotide sequence set forth in SEQ ID NO: 37 or the protein-encoding region thereof or a degenerate nucleotide sequence thereto;
 - (xiii) the nucleotide sequence set forth in SEQ ID NO: 38 or the protein-encoding region thereof or a degenerate nucleotide sequence thereto;

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region thereof or a degenerate nucleotide sequence thereto;

(xiv) the nucleotide sequence set forth in SEQ ID NO: 11 or the protein-encoding region thereof or a degenerate nucleotide sequence thereto;

(xv) a nucleotide sequence which encodes a wheat starch synthase polypeptide as hereinbefore defined wherein said nucleotide sequence has at least about 85% identity overall to any one of (i) to (xiv); and

(xvi) a nucleotide sequence which is complementary to any one of (i) to (xv).

2. The isolated nucleic acid molecule according to claim 1 wherein the wheat starch synthase polypeptide further comprises one or more amino acid sequences selected from the group consisting of:

- (a) KVGGLGDVVT;
- (b) GHTVEVILPKY;
- (c) HDWSSAPVAWLYKEHY;
- (d) GILNGIDPDIWDPYTD;
- (e) DVPIVGIIITRLTAQKG;
- (f) NGQVVLLGSA;
- (g) AGSDFIIVPSIFPCGLTQLVAMRYGS;
- (h) TGGLVDTV;
- (i) KTGGLGLVAGA;
- (j) GHRVMVVVPRY;
- (k) NDWHTALLPVYLKAYY;
- (l) GIVNGIDNMEWNPEVD;
- (m) DVPLLGFGRLDGQKG;
- (n) DVQLVMLGTG;

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(o)AGADALLMPSRF(E/V)PCGLNQLYAMAYGT; and

(p)VGG(V/L)RDTV.

3. The isolated nucleic acid molecule according to claim 2 wherein the wheat starch synthase polypeptide comprises at least three of said amino acid sequences selected from the group consisting of (a) to (h).
4. The isolated nucleic acid molecule according to claim 2 wherein the wheat starch synthase polypeptide comprises at least six of said amino acid sequences selected from the group consisting of (i) to (p).
5. The isolated nucleic acid molecule according to claim 1 encoding a wheat starch synthase II polypeptide.
6. The isolated nucleic acid molecule according to claim 1 encoding a wheat starch synthase III polypeptide.
7. An isolated nucleic acid molecule encoding a starch synthase polypeptide which comprises one or more amino acid sequences selected from the group consisting of:
 - (a) GHTVEVILPKY;
 - (b) HDWSSAPVAWLYKEHY;
 - (c) DVPIVGIITRLTAQKG;
 - (d) NGQVVLLGSA;
 - (e)AGSDFIIVPSIFEPGLTQLVAMRYGS;
 - (f)TGGLVDTV;
 - (g) GIVNGIDNMEWNPEVD; and

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(h) AGADALLMPSRF(E/V)PCGLNQLYAMAYGT.

8. The isolated nucleic acid molecule of claim 5 encoding a wheat starch synthase II polypeptide which comprises an amino acid sequence selected from the group consisting of:
 - (i) SEQ ID NO: 2;
 - (ii) SEQ ID NO: 4;
 - (iii) SEQ ID NO: 6; and
 - (iv) a homologue of any one of (i) to (iii) having at least about 85% identity thereto.
9. The isolated nucleic acid molecule of claim 6 encoding a wheat starch synthase III polypeptide which comprises an amino acid sequence selected from the group consisting of:
 - (i) SEQ ID NO: 8;
 - (ii) SEQ ID NO: 10; and
 - (iii) a homologue of (i) or (ii) having at least about 85% identity thereto.
10. A probe or primer comprising at least about 15 contiguous nucleotides in length derived from the nucleotide sequence according to claim 1.
11. The probe or primer according to claim 10 comprising a nucleotide sequence selected from the group consisting of:
 - (i) the nucleotide sequence set forth in SEQ ID NO: 25;
 - (ii) the nucleotide sequence set forth in SEQ ID NO: 26;
 - (iii) the nucleotide sequence set forth in SEQ ID NO: 27;

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- (iv) the nucleotide sequence set forth in SEQ ID NO: 28;
- (v) the nucleotide sequence set forth in SEQ ID NO: 29;
- (vi) the nucleotide sequence set forth in SEQ ID NO: 30;
- (vii) the nucleotide sequence set forth in SEQ ID NO: 31;
- (viii) the nucleotide sequence set forth in SEQ ID NO: 32;
- (ix) the nucleotide sequence set forth in SEQ ID NO: 33;
- (x) the nucleotide sequence set forth in SEQ ID NO: 34;
- (xi) a nucleotide sequence which encodes an amino acid sequence selected from the group consisting of:

- (a) KVGGLGDVVTs;
- (b) GHTVEVILPKY;
- (c) HDWSSAPVAWLYKEHY;
- (d) GILNGIDPDIWDPYTD;
- (e) DVPIVGIITRLTAQKG;
- (f) NGQVLLGSA;
- (g) AGSDFIIVPSIFPCGLTQLVAMRYGS;
- (h) TGGLVDTV;
- (i) KTGGLGDVAGA;
- (j) GHRVMVVVPKY;
- (k) NDWHTALLPVYLKAYY;
- (l) GIVNGIDNMEWNPEVD;
- (m) DVPLLGFGRLDGQKG;
- (n) DVQLVMLGTG;
- (o) AGADALLMPSRF(E/V)PCGLNQLYAMAYGT; and

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(p)VGG(V/L)RDTV;

(xii) a nucleotide sequence comprising at least about 15 contiguous nucleotides of an intron region of SEQ ID NO: 37;

(xiii) a nucleotide sequence comprising at least about 15 contiguous nucleotides of an intron region of SEQ ID NO: 38; and

(xiv) a nucleotide sequence which is complementary to any one of (i) to (xiii).

12. An isolated or recombinant polypeptide, protein or enzyme comprising an amino acid sequence selected from the following:

(i) the amino acid sequence set forth in SEQ ID NO: 2 or the mature protein region thereof;

(ii) the amino acid sequence set forth in SEQ ID NO: 4 or the mature protein region thereof;

(iii) the amino acid sequence set forth in SEQ ID NO: 6 or the mature protein region thereof;

(iv) the amino acid sequence set forth in SEQ ID NO: 8 or the mature protein region thereof;

(v) the amino acid sequence set forth in SEQ ID NO: 10 or the mature protein region thereof;

(vi) a wheat starch synthase polypeptide having at least about 85% identity overall to any one of (i) to (v).

13. The isolated or recombinant polypeptide according to claim 12 further comprising one or more amino acid sequences selected from the group consisting of:

(a) KVGGLGDVVTs;

(b) GHTVEVILPKY;

(c) HDWSSAPVAWLYKEHY;

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(d) GILNGIDPDIWDPYTD;

(e) DVPIVGIITRLTAQKG;

(f) NGQVLLGSA;

(g)AGSDFIIVPSIFEPCGLTQLVAMRYGS;

(h)TGGLVDTV;

(i) KTGGLGDVAGA;

(j) GHRVMVVVPY;

(k) NDWHTALLPVYLKAYY;

(l) GIVNGIDNMEWNPEVD;

(m) DVPLLGFIRLDGQKG;

(n) DVQLVMLGTG;

(o)AGADALLMPSRF(E/V)PCGLNQLYAMAYGT; and

(p)VGG(V/L)RDTV.

14. The isolated or recombinant polypeptide according to claim 13 wherein the wheat starch synthase polypeptide comprises at least three of said amino acid sequences selected from the group consisting of (a) to (h).
15. The isolated or recombinant polypeptide according to claim 13 wherein the wheat starch synthase polypeptide comprises at least six of said amino acid sequences selected from the group consisting of (i) to (p).
16. The isolated or recombinant polypeptide according to claim 12 encoding a wheat starch synthase II polypeptide.

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17. The isolated or recombinant polypeptide according to claim 12 encoding a wheat starch synthase III polypeptide.
18. An isolated or recombinant starch synthase polypeptide which comprises one or more amino acid sequences selected from the group consisting of:
 - (a) GHTVEVILPKY;
 - (b) HDWSSAPVAWLYKEHY;
 - (c) DVPIVGIIITRLTAQKG;
 - (d) NGQVVLLGSA;
 - (e) AGSDFIIVPSIFPCGLTQLVAMRYGS;
 - (f) TGGLVDTV;
 - (g) GIVNGIDNMEWNPEVD; and
 - (h) AGADALLMPSRF(E/V)PCGLNQLYAMAYGT.
19. The isolated or recombinant polypeptide according to claim 16 consisting of a wheat starch synthase II polypeptide which comprises an amino acid sequence selected from the group consisting of:
 - (i) SEQ ID NO: 2;
 - (ii) SEQ ID NO: 4;
 - (iii) SEQ ID NO: 6; and
 - (iv) a homologue of any one of (i) to (iii) having at least about 85% identity thereto.
20. The isolated or recombinant polypeptide according to claim 17 consisting of a wheat starch synthase III polypeptide which comprises an amino acid sequence selected from the group consisting of:

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- (i) SEQ ID NO: 8;
 - (ii) SEQ ID NO: 10; and
 - (iii) a homologue of (i) or (ii) having at least about 85% identity thereto.
21. The isolated or recombinant polypeptide according to claim 12 substantially free of conspecific or non-specific proteins.
22. A method comprising:
- (i) hybridising single-stranded or double-stranded mRNA, cDNA or genomic DNA with a nucleotide sequence selected from the group consisting of:
 - (a) the nucleotide sequence according to any one of claims 1 to 9;
 - (b) a probe or primer derived from a nucleotide sequence according to subparagraph (a) and comprising at least about 15 contiguous nucleotides of said nucleotide sequence in length; and
 - (ii) detecting the hybridised mRNA, cDNA or genomic DNA using a detecting means.
23. The method according to claim 22 wherein the detecting means consists of a reporter molecule covalently attached to the probe or primer molecule.
24. The method according to claim 22 wherein the detecting means consists of a polymerase chain reaction.
25. The method according to claim 22 wherein the probe or primer comprises a nucleotide sequence selected from the group consisting of:
- (i) the nucleotide sequence set forth in SEQ ID NO: 25;

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- (ii) the nucleotide sequence set forth in SEQ ID NO: 26;
- (iii) the nucleotide sequence set forth in SEQ ID NO: 27;
- (iv) the nucleotide sequence set forth in SEQ ID NO: 28;
- (v) the nucleotide sequence set forth in SEQ ID NO: 29;
- (vi) the nucleotide sequence set forth in SEQ ID NO: 30;
- (vii) the nucleotide sequence set forth in SEQ ID NO: 31;
- (viii) the nucleotide sequence set forth in SEQ ID NO: 32;
- (ix) the nucleotide sequence set forth in SEQ ID NO: 33;
- (x) the nucleotide sequence set forth in SEQ ID NO: 34;
- (xi) a nucleotide sequence which encodes an amino acid sequence selected from the group consisting of:

- (a) KVGGLGDVWTS;
- (b) GHTVEVILPKY;
- (c) HDWSSAPVAWLYKEHY;
- (d) GILNGIDPDIWDPYTD;
- (e) DVPIVGIIITRLTAQKG;
- (f) NGQVVLLGSA;
- (g) AGSDFIIVPSIFEPCGLTQLVAMRYGS;
- (h) TGGLVDTV;
- (i) KTGGLGDVAGA;
- (j) GHRVMVVVPRY;
- (k) NDWHTALLPVYLKAYY;
- (l) GIVNGIDNMEWNPEVD;
- (m) DVPLLGFGRLDGQKG;

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(n) DVQLVMLGTG;

(o)AGADALLMPSRF(E/V)PCGLNQLYAMAYGT; and

(p)VGG(V/L)RDTV;

(xii) a nucleotide sequence comprising at least about 15 contiguous nucleotides of an intron region of SEQ ID NO: 37;

(xiii) a nucleotide sequence comprising at least about 15 contiguous nucleotides of an intron region of SEQ ID NO: 38; and

(xiv) a nucleotide sequence which is complementary to any one of (i) to (xiii).

26. A method of assaying for the presence or absence of a wheat starch synthase polypeptide in a plant or a plant extract or isolated nucleic acid sample, said method at least comprising performing the method according to any one of claims 22 to 25.
27. The method according to claim 26 further comprising preparing the plant extract or nucleic acid sample.
28. A method of marker-assisted breeding and/or selection of a plant at least comprising performing the method according to any one of claims 22 to 25.
29. The method according to claim 28 further comprising selecting a plant which expresses a desirable wheat starch synthase characteristic.
30. The method according to claim 28 further comprising crossing a plant which expresses a desirable wheat starch synthase characteristic to another plant.
31. The method according to claim 30 further comprising selecting progeny of the cross

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which expresses a desirable wheat starch synthase characteristic.

32. A plant produced by the method according to any one of claims 28 to 31 wherein said plant expresses a wheat starch synthase polypeptide at a desired level detectable using said method.
33. A method of modifying the starch content and/or starch composition of one or more tissues or organs of a plant, comprising expressing in said plant a nucleic acid molecule for a time and under conditions sufficient for the enzyme activity of one or more starch synthase isoenzymes to be modified, wherein said nucleic acid molecule is selected from the group consisting of:
 - (i) the isolated nucleic acid molecule according to any one of claims 1 to 9;
 - (ii) a fragment of (i) which comprises a nucleotide sequence capable of being expressed to down-regulate the expression of an endogenous wheat starch synthase isoenzyme of said plant; and
 - (iii) a fragment of (i) which encodes a functional wheat starch synthase isoenzyme of said plant.
34. The method according to claim 33 wherein the fragment at sub-paragraph (ii) is an antisense molecule, ribozyme molecule, co-suppression molecule, or gene-targeting molecule.
35. The method according to claim 33 further comprising introducing the nucleic acid molecule to an isolated plant cell, tissue, organ, or organelle.
36. The method according to claim 35 further comprising regenerating an intact plant from the isolated plant cell, tissue, organ, or organelle carrying the introduced nucleic acid molecule.

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37. The method according to claim 35 wherein the nucleic acid molecule is introduced to the plant cell, tissue, organ, or organelle by introgression.
38. The method according to claim 35 wherein the nucleic acid molecule is introduced to the plant cell, tissue, organ, or organelle by transformation means.
39. An isolated promoter sequence comprising a nucleotide sequence selected from the group consisting of:
 - (i) nucleotides 1 to about 287 of SEQ ID NO: 11;
 - (ii) nucleotides 1 to about 1416 of SEQ ID NO: 37;
 - (iii) nucleotides 1 to about 973 of SEQ ID NO: 38;
 - (iv) a fragment of any one of (i) to (iii) capable of conferring expression on a heterologous gene in a monocotyledonous plant cell, tissue or organ; and
 - (v) a complementary nucleotide sequence to any one of (i) to (iv).
40. The isolated promoter sequence according to claim 39 that is operable in the endosperm.
41. A plant carrying the isolated nucleic acid molecule according to any one of claims 1 to 9 as an exogenous complement to its genome.
42. A progeny of the plant according to claim 41 wherein said progeny carries the introduced nucleic acid molecule.
43. A propagule of the plant according to claim 41 or 42 wherein said propagule carries the

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introduced nucleic acid molecule present in said plant.

44. A gene construct or vector which comprises the isolated nucleic acid molecule according to any one of claims 1 to 9 and one or more origins of replication.
45. The gene construct according to claim 44 further comprising a promoter sequence in operable connection with said isolated nucleic acid molecule.
46. A gene construct or vector which comprises the probe or primer according to claim 10 or 11 and one or more origins of replication.
47. A modified starch derived from the plant according to claim 32 or 41 wherein said starch is modified by virtue of the use of the isolated nucleic acid according to claim 1 to produce said plant.
48. A modified starch derived from the progeny according to claim 42 wherein said starch is modified by virtue of the use of the isolated nucleic acid according to claim 1 to produce said progeny.
49. A modified starch derived from the propagule according to claim 43 wherein said starch is modified by virtue of the use of the isolated nucleic acid according to claim 1 to produce said propagule.
50. A food product comprising the modified starch according to any one of claims 47 to 49.
51. The food product according to claim 50 consisting of flour or a flour-based food product.

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52. The food product according to claim 50 or 51 selected from the group consisting of: flour-based sauce; leavened bread; unleavened bread; pasta, noodle; cereal; snack food; cake; and pastry.
53. Use of the modified starch according to any one of claims 47 to 49 in the preparation of a food product for consumption by an animal or human.
54. A modified protein derived from the plant according to claim 32 or 41 wherein said protein is modified by virtue of the use of the isolated nucleic acid according to claim 1 to produce said plant.
55. A modified protein derived from the progeny according to claim 42 wherein said protein is modified by virtue of the use of the isolated nucleic acid according to claim 1 to produce said progeny.
56. A modified protein derived from the propagule according to claim 43 wherein said protein is modified by virtue of the use of the isolated nucleic acid according to claim 1 to produce said propagule.
57. A non-food product comprising the modified protein according to any one of claims 54 to 56.
58. The non-food product according to claim 57 selected from the group consisting of: films; coatings; adhesives; building materials; and packaging materials.
59. Use of the modified protein according to any one of claims 54 to 56 in the preparation of a non-food product.

PCT

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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|---|---|---|
| <p>(51) International Patent Classification ⁷ : C12N 15/54, 15/11, 9/10, C12Q 1/48, 1/68, A01H 1/00, 5/00, C08B 3/02</p> | <p>A1</p> | <p>(11) International Publication Number: WO 00/66745 (43) International Publication Date: 9 November 2000 (09.11.00)</p> |
| <p>(21) International Application Number: PCT/AU00/00385 (22) International Filing Date: 28 April 2000 (28.04.00) (30) Priority Data: PQ0052/99 29 April 1999 (29.04.99) AU (71) Applicants (for all designated States except US): COMMON-WEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION [AU/AU]; Limestone Avenue, Campbell, Australian Capital Territory 2601 (AU). GOODMAN FIELDER LIMITED [AU/AU]; Level 42 Grosvenor Place, Sydney, New South Wales 2000 (AU). GROUPE LIMAGRAIN PACIFIC PTY LTD [AU/AU]; Level 31, 1 O'Connell Street, Sydney, New South Wales 2000 (AU). (72) Inventors; and (75) Inventors/Applicants (for US only): MORELL, Matthew [AU/AU]; 33 Wangara Street, Aranda, Australian Capital Territory 2614 (AU). LI, Zhongyi [AU/AU]; 63 Campaspe Circuit, Kaleen, Australian Capital Territory 2617 (AU). RAHMAN, Sadequr [AU/AU]; 46 Scarlett Street, Melba, Australian Capital Territory 2615 (AU). APPELS, Rudolph [AU/AU]; 40 Gingara Street, Aranda, Australian Capital Territory 2614 (AU).</p> | <p>(74) Agents: OLIVE, Mark, R. et al.; Davies Collison Cave, 1 Little Collins Street, Melbourne, Victoria 3000 (AU). (81) Designated States: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published With international search report.</p> | |
| <p>(54) Title: NOVEL GENES ENCODING WHEAT STARCH SYNTHASES AND USES THEREFOR (57) Abstract The present invention provides isolated nucleic acid molecules encoding wheat starch synthases, and probes and primers derived therefrom, which are useful in the modification of plant starch content and/or composition, and for screening plant lines to determine the presence of natural and/or induced mutations in starch synthase genes which affect starch content and/or composition. More particularly, the isolated nucleic acid molecules of the present invention further provide for the screening-assisted breeding of plants having desirable starch content and/or composition, in addition to providing for the direct genetic manipulation of plant starch content and/or composition.</p> | | |

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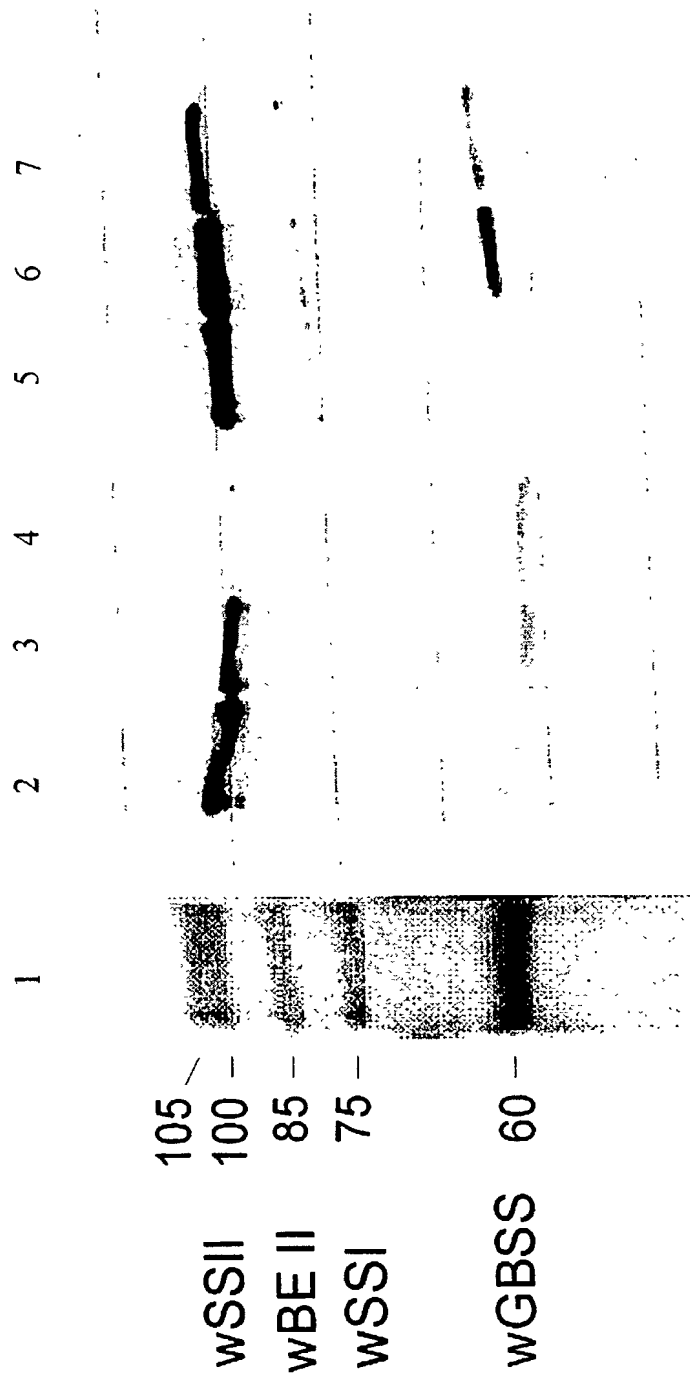


FIGURE 1

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| |
|-----------|
| FIGURE 2A |
| FIGURE 2B |
| FIGURE 2C |
| FIGURE 2D |
| FIGURE 2E |
| FIGURE 2F |
| FIGURE 2G |
| FIGURE 2H |
| FIGURE 2I |
| FIGURE 2J |
| FIGURE 2K |
| FIGURE 2L |
| FIGURE 2M |
| FIGURE 2N |
| FIGURE 2O |

FIGURE 2

1 50
WSSIIB ATTTCCTCGG CCTGACCCCG TCGGTTTACC CCACACAGAG CACACTCCAG
WSSIID ~~~~~~
WSSIIA ~~~~~~
51 100
WSSIIB TCCAGTCCAG CCCACTGCCG CGCTACTCCC CACTCCCACT GCCACCACCT
WSSIID ~~~~~~
WSSIIA ~~~~~~GCT GCCACCACCT
101 150
WSSIIB CCGCCTGCGC CGCGCTCTGG GCGGACCAAC CCGGCGCATCG TATCACGATC
WSSIID ~~~~~~
WSSIIA CCGCCTGCGC CGCGCTCTGG GCGGAGGACC AACCCGCGCA TCGTACCATC
151 200
WSSIIB ACCCACCCTCG ATCCCGGCCG CCGCCATGTC GTCGGCGGTC GCGTCCGCCG
WSSIID ~~~~~~
WSSIIA GCCCGCCCTCG ATCCCGGCCG CCGCCATGTC GTCGGCGGTC GCGTCCGCCG

FIGURE 2A


```
250
WSSIIB CGTCCTTCCT CGCGCTCGCG TCCGCCTCCC CCGGGAGATC ACGGAGGAGG
WSSIID ~~~~~~
WSSIIA CGTCCTTCCT CGCGCTCGCC TCCGCCTCCC CCGGGAGATC ACGCAGGCGG

300
WSSIIB ACGAGGGTGA GCGGCTCGCC ACCCCACACC GGGGCTGGCA GGTGCACTG
WSSIID ~~~~~~
WSSIIA GCGAGGGTGA GCGGCGCGCC ACCCCACGCC GGGGCCGGCA GGTGCACTG

350
WSSIIB GCCGCCGTCG CCGCCGCAGC GCACGGCTCG CGACGGAGCG GTGGCCGCGC
WSSIID ~~~~~~
WSSIIA GCCGCCGTCG CCGCCGCAGC GCACGGCTCG CGACGGAGGT GTGGCCGCGC

400
WSSIIB GCGCCGCCGG GAAGAAGGAC GCGGGGAT.. CGACGACGC CGGCCCCGCG
WSSIID ~~~~~~
WSSIIA GCGCCGCCGG GAAGAAGGAC GCGAGGGTCG ACGACGACGC CGGTCCCGCG
```

FIGURE 2B

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| | | |
|--------|-------------|---|
| 401 | 450 | |
| wSSIIB | AGGCAGCCCC | GCGCACTCCG CCGTGGCGCC GCCACCAAGG TTGCGGAGCG |
| wSSIID | ~~~~~ | ~~~~~ |
| wSSIIA | AGGCAGCCCC | GCGCACGCCG CCGTGGCGCC GcCACCAAGG TCGCGGAGCG |
| 451 | 500 | |
| wSSIIB | GAGGGATCCC | GTCAAGACGC TCGATCGCGA CGCCGCGGAA GGTGGCGCGC |
| wSSIID | ~~~~~ | ~~~~~ |
| wSSIIA | GAGGGATCCC | GTCAAGACGC TCGATCGCGA CGCCGCGGAA GGTGGCGCGC |
| 501 | 550 | |
| wSSIIB | CGTCCCCCGCC | GGCACCGAGG CAGGAGGACG CCCGTCTGCC GAGCATGAAC |
| wSSIID | ~~~~~ | ~~~~~ |
| wSSIIA | CGGCACCGCC | GGCACCGAGG CAGGACGCCG CCCGTCCaCC GAGTATGAAC |
| 551 | 600 | |
| wSSIIB | GGCATGCCCG | TGAACGGTGA AAACAAATCT ACCGGCGGCG GCGGCGCGAC |
| wSSIID | ~~~~~ | ~~~~~ |
| wSSIIA | GGCACGCCCG | TGAACGGTGA GAACAAATCT ACCGGCGGCG GCGGCGCGAC |

FIGURE 2C

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```
601      650
wSSIIB  TAAAGACAGC GGGCTGCCCG CACCCGCACG CGCGCCCCAG CCGTCGAGCC
wSSIID  ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~
wSSIIA  CAAAGACAGC GGGCTgcCCG CACCCGcACG CGCGCCCCAT CCGTCGACCC

651      700
wSSIIB  AGAACAGAGT ACCGGTGAAT GGTGAAAACA AAGCTAACGT CGCCTCGCCG
wSSIID  ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~
wSSIIA  AgAACAgAGT ACCAGTGAAC GGTGAAAACA AAGCTAACGT CGCCTCGCCG

701      750
wSSIIB  CCGACGAGCA TAGCCGAGGT CGCGGCTCCG GATCCCGCAG CTACCATTTT
wSSIID  ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~
wSSIIA  CCGACGAGCA TAGCCGAGGT CGTGGCTCCG GATTCCGCAG CTACCATTTT

751      800
wSSIIB  CATCAGTGAC AAGGCGCCAG AGTCCGTTGT CCCAGCCGAG AAGGgcgcgc
wSSIID  ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~
wSSIIA  CATCAGTGAC AAGGCGCCGG AGTCCGTTGT CCCAGCCGAG AAGCCGCCGC
```

FIGURE 2D

801
wSSIIB CGtCgtcCgg CtcAAATtTc gtgCcCtCgg cttctGctCc cggGtctGAC 850
wSSIID CGTCGTCCGG CTCAAATtTc GAGTCCTCGG CCTCTGCTCC CGGTCTGAC
wSSIIA CGTCGTCCGG CTCAAATtTc GTGgTCTCGG CTTCTGCTCC CAGGCTGGAC
851
wSSIIB actgtCaGCG acGtGGaact TgaActGAAG aAGGgtgCgg tCattgTcaa 900
wSSIID ACTGTCAGCG ACGTGGaACA AGAACTGAAG AAGGTGCGG TCGTTGTCGA
wSSIIA ATTGACAGCG ATGTTGAACC TGAActGAAG AAGGTGCGG TCATCGTCGA
901
wSSIIB aGAAGcTcCa aaCcCaAaAG CTCtTTcGCC GCCCGCAGCA CCCGCTGTAC 950
wSSIID AGAAGCTCCA AAGCCAAAGG CTCtTTcGCC GCctGCAGCc CCCGCTGTAC
wSSIIA AGAAGCTCCA AACCCAAAGG CTCtTTcGCC GCCTGCAGCc CCCGCTGTAC
951
wSSIIB AACAAAGACCT TTGGGACTTC AAGAAATACA TTGGTTTCGA GGAGCCCCGTG 1000
wSSIID AAgAAGACCT TTGGGAtTTC AAGAAATACA TTGGTTTCGA GGAGCCCCGTG
wSSIIA AAGAAGACCT TTGGGACTTC AAGAAATACA TTGGCTTCGA GGAGCCCCGTG

FIGURE 2E

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| | | | | | | |
|--------|-------------|------------|-------------|------------|------------|------|
| 1001 | GAGGCCAAGG | ATGATGGCCG | GGCTGTTGCA | GATGATGCGG | GCTCCTTCGA | 1050 |
| wSSIIB | | | | | | |
| 1001 | GAGGCCAAGG | ATGATGGCCG | GGCTGTTGCA | GATGATGCGG | GCTCCTTCGA | 1050 |
| wSSIID | | | | | | |
| 1001 | GAGGCCAAGG | ATGATGGCTG | GGCTGTTGCA | GATGATGCGG | GCTCCTTCGA | 1050 |
| wSSIIA | | | | | | |
| 1051 | ACACCACCAG | AATCACGATT | CCGGGCCCTTT | GGCAGGGGAG | AACGTCATGA | 1100 |
| wSSIIB | | | | | | |
| 1051 | ACACCACCAG | AATCACGACT | CCGGaCCTTT | GGCAGGGGAG | AAtGTCATGA | 1100 |
| wSSIID | | | | | | |
| 1051 | ACATCACCCAG | AACCATGATT | CCGGACCCTTT | GGCAGGGGAG | AACGTCATGA | 1100 |
| wSSIIA | | | | | | |
| 1101 | ACGTGGTCGT | CGTGGCTGCT | GAATGTTCTC | CCTGGTGCAA | AACAGGTGGT | 1150 |
| wSSIIB | | | | | | |
| 1101 | ACGTGGTCGT | CGTGGCTGCT | GAgTGTTCCTC | CCTGGTGCAA | AACAGGTGGT | 1150 |
| wSSIID | | | | | | |
| 1101 | ACGTGGTCGT | CGTGGCTGCT | GAATGTTCTC | CCTGGTGCAA | AACAGGTGGT | 1150 |
| wSSIIA | | | | | | |
| 1151 | CTTGGAGATG | TTGCCGGTGC | TTTGCCCCAAG | GCTTTGGCGA | AGAGAGGACA | 1200 |
| wSSIIB | | | | | | |
| 1151 | CTgGGAGATG | TTGcgGGTGC | TcTGCCCCAAG | GCTTTGGCaA | AGAGAGGACA | 1200 |
| wSSIID | | | | | | |
| 1151 | CTTGGAGATG | TTGCCGGTGC | TTTGCCCCAAG | GCTTTGGCGA | AGAGAGGACA | 1200 |
| wSSIIA | | | | | | |

FIGURE 2F

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| | | | | | |
|--------|------------|-------------|------------|------------|------------|
| 1201 | 1250 | | | | |
| wSSIIB | TCGTGTTATG | GTTGTGGTAC | CAAGGTATGG | GGACTATGAG | GAAGCCTACG |
| wSSIID | TCGTGTTATG | GTTGTGGTAC | CAAGGTATGG | GGACTATGAa | GAACCTACGg |
| wSSIIA | TCGTGTTATG | GTTGTGGTAC | CAAGGTATGG | GGACTATGAG | GAAGCCTACG |
| 1251 | 1300 | | | | |
| wSSIIB | ATGTCGGAGT | CCGAAAATAC | TACAAGGCTG | CTGGACAGGA | TATGGAAGTG |
| wSSIID | ATGTCGGAGT | CCGAAAATAC | TACAAGGCTG | CTGGACAGGA | TATGGAAGTG |
| wSSIIA | ATGTCGGAGT | CCGAAAATAC | TACAAGGCTG | CTGGACAGGA | TATGGAAGTG |
| 1301 | 1350 | | | | |
| wSSIIB | AATTATTTC | ATGCTTATAT | CGATGGAGTT | GATTTGTGT | TCATTGACGC |
| wSSIID | AATTATTTC | ATGCTTaTAT | CGATGGAGTT | GATTTGTGT | TCATTGACGC |
| wSSIIA | AATTATTTC | ATGCTTATAT | CGATGGAGTT | GATTTGTGT | TCATTGACGC |
| 1351 | 1400 | | | | |
| wSSIIB | TCCTCTCTTC | CGACACCGCC | AGGAAGACAT | TTATGGGGGC | AGCAGACAGG |
| wSSIID | TCCTCTCTTC | CGACACCGGAG | AGGAAGACAT | TTATGGGGGC | AGCAGACAGG |
| wSSIIA | TCCTCTCTTC | CGACACCGCC | AGGAAGACAT | TTATGGGGGC | AGCAGACAGG |

FIGURE 2G

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| | | | | | |
|--------|------------|------------|------------|-------------|-------------|
| 1401 | 1450 | | | | |
| wSSIIB | AAATTATGAA | GCGCATGATT | TTGTTCTGCA | AGGCCGCTGT | CGAGGTTCCA |
| wSSIID | AAATTATGAA | GCGCATGATT | TTGTTCTGCA | AGGCCGCTGT | TGAGGTTCCA |
| wSSIIA | AAATTATGAA | GCGCATGATT | TTGTTCTGCA | AGGCCGCTGT | CGAGGTTCCCT |
| 1451 | 1500 | | | | |
| wSSIIB | TGGCACGTTT | CATGCGGCGG | TGTCCCTTAT | GGGATGGAA | ATCTGGTGTT |
| wSSIID | TGGCACGTTT | CATGCGGCGG | TGTCCCTTAT | GGGATGGAA | ATCTGGTGTT |
| wSSIIA | TGGCACGTTT | CATGCGGCGG | TGTCCCTTAT | GGGATGGAA | ATCTGGTGTT |
| 1501 | 1550 | | | | |
| wSSIIB | TATTGCAAAT | GATTGGCACA | CGGCACTCCT | GCCTGTCCTAT | CTGAAAGCAT |
| wSSIID | TATTGCAAAT | GATTGGCACA | CGGCACTCCT | GCCTGTCCTAT | CTGAAAGCAT |
| wSSIIA | TATTGCAAAT | GATTGGCACA | CGGCACTCCT | GCCTGTCCTAT | CTGAAAGCAT |
| 1551 | 1600 | | | | |
| wSSIIB | ATTACAGGGA | CCATGGTTTG | ATGCAGTACA | CTCGGTCCAT | TATGGTGATA |
| wSSIID | ATTACAGGGA | CCATGGTTTG | ATGCAGTACA | CTCGGTCCAT | TATGGTGATA |
| wSSIIA | ATTACAGGGA | CCATGGTTTG | ATGCAGTACA | CTCGGTCCAT | TATGGTGATA |

FIGURE 2H

| | | | | | | | |
|------|--------|------------|------------|------------|------------|------|------------|
| 1601 | WSSIIB | CATAACATCG | CTCACCAGGG | CCGTGGCCCA | GTAGATGAGT | 1650 | TCCCGTTCAC |
| | WSSIID | CATAACATCG | CTCACCAGGG | CCGTGGCCCT | GTAGATGAAT | | TCCCGTTCAC |
| | WSSIIA | CATAACATCG | CGCACCAGGG | CCGTGGCCCA | GTAGATGAAT | | TCCCGTTCAC |
| 1651 | WSSIIB | CGAGTTGCCT | GAGCACTACC | TGGAACACTT | CAGACTGTAC | 1700 | GACCCCGTGG |
| | WSSIID | CGAGTTGCCT | GAGCACTACC | TGGAACACTT | CAGACTGTAC | | GACCCCGTGG |
| | WSSIIA | CGAGTTGCCT | GAGCACTACC | TGGAACACTT | CAGACTGTAC | | GACCCCGTGG |
| 1701 | WSSIIB | GTGGTGAACA | CGCCAACTAC | TTCGCCGCCG | GCCTGAAGAT | 1750 | GGCGGACCAG |
| | WSSIID | GTGGTGAACA | CGCCAACTAC | TTCGCCGCCG | GCCTGAAGAT | | GGCGGACCAG |
| | WSSIIA | GTGGTGAACA | CGCCAACTAC | TTCGCCGCCG | GCCTGAAGAT | | GgCGGACCAG |
| 1751 | WSSIIB | GTGTCGTGG | TGAGCCCCGG | GTACCTGTGG | GAGCTGAAGA | 1800 | CGGTGGAGGG |
| | WSSIID | GTGTCGTGG | TGAGCCCCGG | GTACCTGTGG | GAGCTGAAGA | | CGGTGGAGGG |
| | WSSIIA | GTGTCGTGG | TGAGCCCCGG | GTACCTGTGG | GAGCTCAAGA | | CGGTGGAGGG |

FIGURE 2I

1801
wSSIIB CGGCTGGGGG CTTACGACA TCATACGGCA GAACGACTGG AAGACCCGCG 1850
wSSIID CGGCTGGGGG CTTACGACA TCATACGGCA GAACGACTGG AAGACCCGCG
wSSIIA CGGCTGGGGG CTTACGACA TCATACGGCA GAACGACTGG AAGACCCGCG

1851
wSSIIB GCATCGTGAA CGGCATCGAC AACATGGAGT GGAACCCCGA GGTGGACGTC 1900
wSSIID GCATCGTCAA CGGCATCGAC AACATGGAGT GGAACCCCGA GGTGGACGCC
wSSIIA GCATCGTCAA CGGCATCGAC AACATGGAGT GGAACCCCGA GGTGGACGTC

1901
wSSIIB CACCTCAAGT CGGACGGCTA CACCAACTTC TCCCTGGGGA CGCTGGACTC 1950
wSSIID CACCTCAAGT CGGACGGCTA CACCAACTTC TCCCTGAGGA CGCTGGACTC
wSSIIA CACCTCAAGT CGGACGGCTA CACCAACTTC TCCCTGGGGA CGCTGGACTC

1951
wSSIIB CGGCAAGCGG CAGTGCAAGG AGGCCCTGCA GCGGAGAGTG GGCCTGCAGG 2000
wSSIID CGGCAAGCGG CAGTGCAAGG AGGCCCTGCA GCGGAGAGTG GGCCTGCAGG
wSSIIA CGGCAAGCGG CAGTGCAAGG AGGCCCTGCA GCGGAGAGTG GGCCTGCAGG

FIGURE 2J

Title: Genes Encoding Wheat Starch Synthases
and Uses Therefor

Inventors: Morrell et al.

Filing Date: October 29, 2001

WO 00/66745

T/AU00/00385

| | |
|--------|--|
| 2001 | 2050 |
| wSSIIB | TCGCGGGCGA CGTGCCGCTG CTCGGCTTCA TCGGGCGCCT GGACGGGCAG |
| wSSIID | TCGCGGGCGA CGTGCCGCTG CTCGGCTTCA TCGGGCGCCT GGACGGGCAG |
| wSSIIA | TCGCGGGCGA CGTGCCGCTG CTCGGCTTCA TCGGGCGCCT GGACGGGCAG |
| 2051 | 2100 |
| wSSIIB | AAGGGCGTGG AGATCATCGC GGACGCGATG CCCTGGATCG TGAGCCAGGA |
| wSSIID | AAGGGCGTGG AGATCATCGC GGACGCGATG CCCTGGATCG TGAGCCAGGA |
| wSSIIA | AAGGGCGTGG AGATCATCGC GGACGCGATG CCCTGGATCG TGAGCCAGGA |
| 2101 | 2150 |
| wSSIIB | CGTGCAGCTG GTCATGCTGG GCACCGGGCG CCACGACCTG GAGGGCATGC |
| wSSIID | CGTGCAGCTG GTCATGCTGG GCACCGGGCG CCACGACCTG GAGGGCATGC |
| wSSIIA | CGTGCAGCTG GTCATGCTGG GCACCGGGCG CCACGACCTG GAGGGCATGC |
| 2151 | 2200 |
| wSSIIB | TGCGGCACTT CGAGCGGGAG CACCACGACA AGTGCGCGG GTGGGTGGGG |
| wSSIID | TGCGGCACTT CGAGCGGGAG CACCACGACA AGTGCGCGG GTGGGTGGGG |
| wSSIIA | TGCGGCACTT CGAGCGGGAG CACCACGACA AGTGCGCGG GTGGGTGGGG |

FIGURE 2K

2201
wSSIIB TTCTCCGTGC GGCTGGCGCA CCGGATCACG GCCGGCGCCG ACGGCTCCT 2250
wSSIID TTCTCCGTGC GCCTGGCGCA CCGGATCACG GCGGGGCGCG ACGGCTCCT
wSSIIA TTCTCCGTgc GcCTGGCGCA CCGGATCACG GCGGGCGCCG ACGGCTCct

2251
wSSIIB CATGCCCTCC CGGTCGAGC CGTGCGGACT GAACCAAGCTC TACGCCATGG 2300
wSSIID CATGCCCTCC CGGTCGTGC CGTGCGGGCT GAACCAAGCTC TACGCCATGG
wSSIIA CATGCCCTCC CGGTCGAgC CGTGCGGGTT GAACCAAGCTt TACGCCATGG

2301
wSSIIB CCTACGGCAC CGTCCCCGTC GTGCATGCCG TCGGTGGCCT GAGGGACACC 2350
wSSIID CCTACGGCAC CGTCCCCGTC GTGCACGCCG TCGCGGGCCT CAGGGACACC
wSSIIA CCTACGGCAC CGTCCCCGTC GTGCACGCCG TCGCGGGGT GAGGGACACC

2351
wSSIIB GTGCCGCCGT TCGACCCCTT CAACCACTCC GGGCTCGGGT GGACGTTCGA 2400
wSSIID GTGCCGCCGT TCGACCCCTT CAACCACTCC GGGCTCGGGT GGACGTTCGA
wSSIIA GTGCCGCCGT TCGACCCCTT CAACCACTCC GGCCTCGGGT GGACGTTCGA

FIGURE 2L

2401
wSSIIB CCGCGCAGAG GCGCAGAAGC TGATCGAGGC GCTCGGGCAC TGCCTCCGCA 2450
wSSIID CCGCGCCCGAG GCGCACAAGC TGATCGAGGC GCTCGGGCAC TGCCTCCGCA
wSSIIA CCGCGCCCGAG GCGCACAAGC TGATCGAGGC GCTCGGGCAC TGCCTCCGCA

2451
wSSIIB CCTACCGGGA CTACAAGGAG AGCTGGAGGG GGCTCCAGGA GCGCGGCATG 2500
wSSIID CCTACCGGGA CTACAAGGAG AGCTGGAGGG CCCTCCAGGA GCGCGGCATG
wSSIIA CCTACCGGGA CTACAAGGAG AGCTGGAGGG GGCTCCAGGA GCGCGGCATG

2501
wSSIIB TCGCAGGACT TCAGCTGGGA GCATGCCGCC AAGCTCTACG AGGACGTCCT 2550
wSSIID TCGCAGGACT TCAGCTGGGA GCATGCCGCC AAGCTCTACG AGGACGTCCT
wSSIIA TCGCAGGACT TCAGCTGGGA GCATGCCGCC AAGCTCTACG AGGACGTCCT

2551
wSSIIB CGTCAAGGCC AAGTACCAGT GGTGAACGCT AGCTGCTAGC CGGTCCAGCC 2600
wSSIID CGTCAAGGCC AAGTACCAGT GGTGAACGCT AGCTGCTAGC CGGTCCAGCC
wSSIIA CcTCAAGGCC AAGTACCAGT GGTGAACGCT AGCTGCTAGC CGcTCCAGCC

FIGURE 2M

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2601      wSSIIB      ...TGCATGA CAGGATGGAA TTGCGCATTG CGCAGGCAGG      2650
          wSSIID      ...TGCATGA CAGGATGGAA CT..GCATTG CGCAGGCAGG
          wSSIIA      CGCATGCGT GCATGcatga gAGGgTGGAa cTGCGCATTG CGcCCGCAGG

2651      wSSIIB      ..... .GGAGCGCCG GCATCCGCCG AGTACAGTGA      2700
          wSSIID      ..... .GGAGCGCCG GCATCCGCCG AGTACAGTGA
          wSSIIA      AAcGTGCCAT ccttctcgat gGGAGCGCCG GCATCCGCCG gGTgCAGTGA

2701      wSSIIB      CAT..GAGGT GTGTGTGGTT GAGACGCTGA TTC.....C GATCTGGTCC      2750
          wSSIID      CAT..GAGGT GTGTGTGGTT GAGACGCTGA TTC.....C AATCCGGCCC
          wSSIIA      CATGAGagGT GTGTGTGGTT GAGACGCTGA TTCCGATCTc gatctGGTCC

2751      wSSIIB      GTAGCAGAGT AGAGCGGAGG TAGGGAAGCG CTCCTTGTTA CAGGTATATG      2800
          wSSIID      GTAGCAGAGT AGAGCGGAGG TATATGGGA TCTTAACTTG GTATTGTAAT
          wSSIIA      GTAGCAGAGT AGAGCGGAGc TAGGGAAGCG CTCCTTGTTg CAGGTATATG
```

FIGURE 2N

2801
WSSIIB GGAATGTTGT TAACTTGGTA TTGTAATTG TTATGTTGTG TGCATTATTA 2850
WSSIID TTGTTATGTT GTGTGCATTA TTACAATGTT GTTACTTATT CTTGTTAAGT
WSSIIA GGAATGTTGT CAACTTGGTA TTGTAGTTG CTATGTTGTa TGCgTTATTA

2851
WSSIIB CAGAGGGCAA CGATCTGCGC CGGCGCACCG GCCCAACTGT TGGGCCGGTC 2900
WSSIID CGGAGGCCAA GGGCGAAAGC TAGCTCACAT GTCTGATGGA TGCAAAAAAA
WSSIIA caatgttgtt acttattctt gtTAAAAAAA AAAAAA AAAA~~~~~

2901
WSSIIB GCACAGCAGC CGTTGGATCC GACCGCCTGG GCCGTTGGAT CCCACCGAAA 2950
WSSIID AAAAAA AAAA~~~~~
WSSIIA ~~~~~~

2951 2965
WSSIIB AAAAAA AAAA
WSSIID ~~~~~~
WSSIIA ~~~~~~

FIGURE 20

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[AU00/00385]

FIGURE 3A

FIGURE 3B

FIGURE 3C

FIGURE 3D

FIGURE 3E

FIGURE 3F

FIGURE 3G

FIGURE 3

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| | | | | | | | | | | |
|---------------------------------|----|-------------|------------|-------------|-------------|------------|------------|------------|------------|-----|
| WSSIIA | 1 | MSSAVASAAS | --- | FLALASA | SP-GRSRRRA | RVSAPPPHAG | AGRL---- | HW | PPWPP-QRTA | 51 |
| WSSIIB | 1 | ***** | --- | ***** | ***** | ***S***T* | ***** | *** | **S*** | 51 |
| WSSIID | | --- | --- | --- | --- | --- | --- | --- | --- | |
| ZSSIIA | 1 | ***AV*SS* | STF***** | *** | **G***--*** | **GSS*F*T* | *-S*SFAFWA | **S**RAPRD | | 57 |
| ZSSIIB | 1 | *PG*-I*SS* | SAFL*PV**S | ***--R***G | S*G*ALRSY* | YSGAELRL** | ARRG*P*DG* | | | 56 |
| PEASSII | 1 | *MLSLG*D*T | VLP*H*KNLK | FTP*KL*TLNG | --DLAFSKGL | GVGRINCGSV | -----R | | | 49 |
| POTSSII | 10 | PVNFIFCDFY | VMENSI*LHS | GNQFHPNLPL | ---LALRPKK | LSLIHGSSRE | -----Q | | | 57 |
| ↓ Transit peptide cleavage site | | | | | | | | | | |
| WSSIIA. | 52 | RDGGVAARAA | GKKDARVDDD | AASARQPRAR | RGGAATKVAE | RRDPVKTLDR | DAAEGGAPAP | | | 111 |
| WSSIIB | 52 | ***A***** | ***GI--** | **p*****L | ***** | ***** | *****S* | | | 110 |
| WSSIID | | --- | --- | --- | --- | --- | --- | | | |
| ZSSIIA | 58 | AALVR*EAE* | *G***PPERS | GDA**L*** | *---NA*SK | *** | ----- | | | 97 |
| ZSSIIB | 57 | -ASVR**A*P | AGG----- | --- | --- | --- | --- | | | 68 |
| PEASSII | 50 | LNHKQHV**V | **SEFADENG | DG*EDDVVNA | TIEKSK**LA | LORELIQQIA | ERKKLVSSID | | | 109 |
| POTSSII | 58 | MWRNQVRVK*T | *ENSGEAA-S | *DESNDALQV | TIEKSK**LA | MQQDLLQQIA | ERRKVVSSIK | | | 116 |

FIGURE 3A

| | | | | | | | | |
|---------|-----|-------------|------------|------------|-------------|--------------|-------------|-----|
| WSSIIA | 112 | PAPRQDAARP | PSMNGTPVNG | ENKSTGGGA | TKDSGLPAPA | RAPHPSTQNR | VPVNGENKAN | 171 |
| WSSIIB | 111 | *****ED**L | *****M**** | ***** | ***** | ***Q**S*** | ***** | 170 |
| WSSIID | | ----- | ----- | ----- | ----- | ----- | ----- | |
| ZSSIIA | 98 | ----- | ----- | -----LQPVG | RYG*ATGNT* | *TGAA*C**A | ALADV*I*SI | 132 |
| ZSSIIB | 69 | ----- | ----- | ----- | -ESEEAAKSS | SSSQAGAVQG | STAKAVDS*S | 97 |
| PEASSII | 110 | SDSIPGLEGN | GVSYESSEKS | LSR----- | ----- | -----DS*P | QKGSSSSGSA | 146 |
| POTSSII | 117 | S-----SL*NA | KGTYDGGSGS | LSDVDIPDVD | KDYNVTVPST | A*TGITDVK | NTPPAISHDF | 172 |
| WSSIIA | 172 | VASPPTSIAE | VVAPDSAATI | SISDKAPESV | VPAEKPPPPSS | GSNFVVSASA | PRLDIDSDVE | 231 |
| WSSIIB | 171 | ***** | *A***P**** | ***** | *****A***** | *****P***** | *GS*TV***** | 230 |
| WSSIID | 203 | ----- | ----- | ----- | ----- | *****ES***** | *GS*TV***** | 231 |
| ZSSIIA | 134 | **A****VK | FP**GYRMIL | PSG*I**T* | L**P*--LH | E*PA*DGD*N | --GIAPPT** | 188 |
| ZSSIIB | 99 | PPN*L**APK | QSQAAMQNG | TSGGSSASTA | A*VSG*KADH | P*AP*TKREI | DASAVKPEPA | 158 |
| PEASSII | 147 | *ETKR--WHC | FQ-----LC | RSKETETWA* | SSVGINQGFED | EIEKKND*VK | ASSKLHFNEQ | 199 |
| POTSSII | 173 | *E*KREIKRD | LADERAPPLS | RS*IT*SSQI | SSTVSSK--R | TL*VPPETPK | SSQETLL**N | 230 |

FIGURE 3B

| | | | | | | | |
|---------|-----|------------|-------------|------------|------------|-----------------------|-----|
| WSSIIA | 232 | PELKKGAVIV | EEAPNPKALS | PPAAPAVQED | LWDFKKYIGF | WSSIIP1 Region | 291 |
| WSSIIB | 231 | L***** | K***** | *****Q* | ***** | EEPVEAKDDG WAVADDAGSF | 290 |
| WSSIID | 232 | Q*****V* | *****K***** | ***** | ***** | *****R***** | 291 |
| ZSSIIA | 189 | * | ----- | -----L**A | T***** | *****R***** | 291 |
| ZSSIIB | 159 | GDDARPVESI | ----- | ----- | ----- | D**D*****S RVG***** | 224 |
| PEASSII | 200 | IKN*LYERPD | TKDIS--SSI | R----- | ----- | A**D**A*- A*P*T**AAS | 188 |
| POTSSII | 231 | SRKSLVD*PG | KKIQSYMPSL | R----- | ----- | KFENFEGANE PSSKEV*NEA | 242 |
| | | | | | ----- | HVEQRNENLE GSS*EANEET | 277 |

| | | | | | | | |
|---------|-----|------------|--------------|------------|------------|------------|------------|
| WSSIIA. | 292 | EHQNHHD--S | GPLAGENVMN | VVVVAAECSP | WCKTGGLGDV | Region 1 | Region 2 |
| WSSIIB | 291 | ***** | ***** | ***** | ***** | AGALPKALAK | RGHRVMVVVP |
| WSSIID | 292 | ***** | ***** | ***** | ***** | ***** | ***** |
| ZSSIIA | 225 | **YGDN*--* | ***** | ***** | ***** | ***** | ***** |
| ZSSIIB | 189 | APYDRE*NEP | *****P***** | *****S**A* | F***** | V***** | ***** |
| PEASSII | 243 | *NFESGGEKP | P*****T***** | IIL*S**A* | *S***** | V***** | *****I* |
| POTSSII | 278 | *DPV*I*EKP | P*****T***** | IIL*S**A* | *S***** | ***** | *****I*A* |
| | | | | | ***** | ***** | *****A* |

FIGURE 3C

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Sgp-1 Peptide 3

| | | | | | | | | |
|---------|-----|---------------|------------|-------------|------------|------------|-----------|-----|
| WSSIIA | 350 | RYGDYEEAYD | VGVRKYYKAA | GQDMEVNYEH | AYIDGVDFVF | IDAPLFRHRQ | EDIYGSRQE | 409 |
| WSSIIB | 349 | ***** | ***** | ***** | ***** | ***** | ***** | 408 |
| WSSIID | 350 | *****PT* | ***** | ***** | ***** | *****E | ***** | 409 |
| ZSSIIA | 283 | *****VF* | ***** | ***** | ***** | ***** | ***** | 342 |
| ZSSIIB | 249 | *****A**R* | L**RR**V* | *****S**T** | S***** | VE**P**H | NN**E*LD | 308 |
| PEASSII | 303 | H**N**A**H* | I**R**V* | *****T** | T*****I** | **S*I**NLE | SN**N*LD | 362 |
| POTSSII | 338 | *****DN*P*PQ* | S**I**VD | ***VD*T**Q | *LLMDC**** | *HSHM**IG | NN**N*VD | 397 |

Region 3

| | | | | | | | | |
|---------|-----|------------|-----------|------------|------------|------------|------------|-----|
| WSSIIA | 410 | IMKRMILFCK | AAVEPWHVP | CGGVPYGDGN | LVFIANDWHT | ALLPVYLKAY | YRDHGLMQYT | 469 |
| WSSIIB | 409 | ***** | ***** | ***** | ***** | ***** | ***** | 468 |
| WSSIID | 410 | ***** | ***** | ***** | ***** | ***** | ***** | 469 |
| ZSSIIA | 343 | ***** | V***** | ***C***** | ***** | ***** | ***** | 402 |
| ZSSIIB | 309 | *L***** | *****YA* | ***TV***** | ***** | ***** | ***N*****A | 368 |
| PEASSII | 363 | *LR**V*** | ***** | ***IC***** | ***** | ***** | *****N** | 422 |
| POTSSII | 398 | *L***V*** | **I***** | ***C***** | ***** | ***A***** | ***N*I*N** | 457 |

FIGURE 3D

WSSIIA 470 RSIMVIHNIA HQGRGPVDEF PFTPEHYL EHFRLYDPVG GEHANYFAAG LKMADQVVVV 529
 WSSIIB 469 *****
 WSSIID 470 *****
 ZSSIIA 404 **VL***** Q**E*****I***** **R**T* 462
 ZSSIIB 369 **VL***** D**K**NI* *D*S*V***** **T**R**T* 428
 PEASSII 423 **VL***** NTVD*SGN** DL*KM***** **F*I***** **T**RI**T* 482
 POTSSII 458 **VL***** SYVD**P**M DP*K***** **F*I***** **T**R**T* 517

Region 4

WSSIIA 530 SPGYLWELKT VEGGWGLHDI IRQNDWKTRG IVNGIDNMEW NPEVDVHLK- SDGYTNFSLG 588
 WSSIIB 529 *****
 WSSIID 530 *****
 ZSSIIA 463 *R**M***** **S*****IN* *****HQ** *K*****R- *****Y**E 521
 ZSSIIB 429 *N**M***** *N*****LQ* *****MS** *A*****H- *****YTFE 487
 PEASSII 483 *H**A***** *NES*****F** *NES*****V*TKD* **QF*AY*T- *****YN*K 541
 POTSSII 518 *H**S***** *NE*****LQ* *****TK** ***L*****PR *****M**Y**D 577

FIGURE 3E

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| Region 5 | | | | | Region 5a | | | | |
|----------|-----|------------|------------|------------|-------------|------------|------------|-----|--|
| WSSIIA | 589 | TLDGKRQCK | EALQRELGLQ | VRADVPLLGF | IGRLDGQKGV | EIIADAMPWI | VSQDVQLVML | 648 | |
| WSSIIB | 588 | ***** | ***** | **G***** | ***** | ***** | ***** | 647 | |
| WSSIID | 588 | ***** | ***** | ***** | ***** | ***** | ***** | 648 | |
| ZSSIIA | 522 | **A***** | A*****E | **D***** | ***** | D**G***** | AG***** | 581 | |
| ZSSIIB | 488 | **T***** | A***Q*** | **D***** | *****H***** | D*****IH** | AG***** | 547 | |
| PEASSII | 542 | **QT***** | A*****P | **E***IIS* | *****H***** | DL**E*I**M | M*H***** | 601 | |
| POTSSII | 578 | **QT**P** | A**K***** | **D***I** | *****P***** | DL**E*V**M | MG***** | 637 | |
| | | | | | | | | | |
| Region 6 | | | | | | | | | |
| WSSIIA | 649 | GTGRHDLESM | LRHFEREHD | KVRGWVGFSV | RLAHRITAGA | DALLMPSRFE | PCGLNQLYAM | 708 | |
| WSSIIB | 648 | *****G* | ***** | ***** | ***** | ***** | ***** | 707 | |
| WSSIID | 649 | ***** | *Q***** | ***** | ***** | *****V | ***** | 708 | |
| ZSSIIA | 582 | ***A***R* | *Q*L***PN | ***** | PM***** | *V***** | ***** | 641 | |
| ZSSIIB | 548 | ***A***D* | **R**S**S* | ***A***** | P***** | *I***** | ***** | 607 | |
| PEASSII | 602 | ***A***Q* | *KE**AQ*C* | *I*S***** | KM*****S | *I***** | ***** | 661 | |
| POTSSII | 638 | ***R***Q* | **Q**CQ*N* | *I***** | KTS***** | *I***** | **A***** | 697 | |

FIGURE 3F

| | | | | | | | | |
|---------|-----|------------------|-------------------|-------------|------------|--------------|-------------|-----|
| WSSIIA | 709 | <u>AYGTPVVHA</u> | <u>VGGVRDTVPP</u> | FDPFNHSGLG | WTFDRAEAKH | LIEALGHCLR | TYRDYKESWR | 768 |
| WSSIIB | 708 | <u>*****</u> | <u>***L***</u> | ***** | *****Q* | ***** | ***** | 767 |
| WSSIID | 709 | <u>*****</u> | <u>***L***</u> | ***** | ***** | ***** | ***F*** | 768 |
| ZSSIIA | 642 | <u>*****</u> | <u>***L***A</u> | ***GDA*** | *****N* | ***** | ***K*G***K | 701 |
| ZSSIIB | 608 | <u>*****</u> | <u>***L***A</u> | *****DT** | *****NR | M*D**S***T | ***N*** | 667 |
| PEASSII | 662 | <u>S*****G</u> | <u>***L***Q*</u> | *N**DE**V* | *****N* | *MA**WN**L | ***K***K**E | 721 |
| POTSSII | 698 | <u>K***I****</u> | <u>***L***Q*</u> | * **LMSQDW* | GPS*****SQ | * **PRIRN**L | ***E**K**E | 757 |

| | | | | | | |
|---------|-----|------------|------------|-------------|---|-----|
| WSSIIA | 769 | GLQERMSQD | FSWEHAAKLY | EDVLLKAKYQ | W | 799 |
| WSSIIB | 768 | ***** | ***** | ***V***** | * | 798 |
| WSSIID | 769 | ***** | ***** | ***V***** | * | 799 |
| ZSSIIA | 702 | S**A***** | L**D***E** | ***V***** | * | 732 |
| ZSSIIB | 668 | ACRA**AE* | L**D***V** | ***V***** | * | 698 |
| PEASSII | 722 | *I***** | L**DN**QQ* | *E**VA***** | * | 752 |
| POTSSII | 759 | *I*T*C*T** | L**DN**QN* | *E**IA***** | * | 788 |

FIGURE 3G

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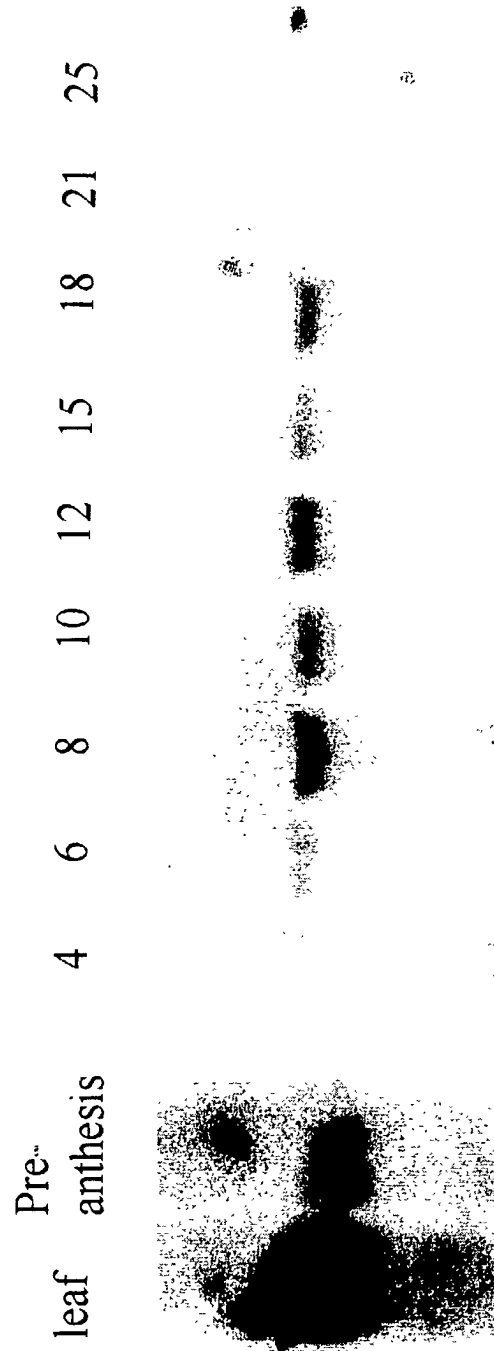


FIGURE 4

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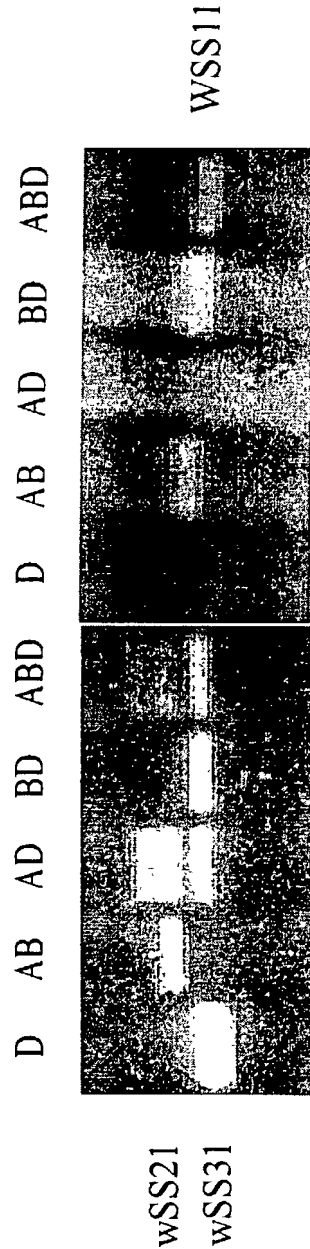


FIGURE 5

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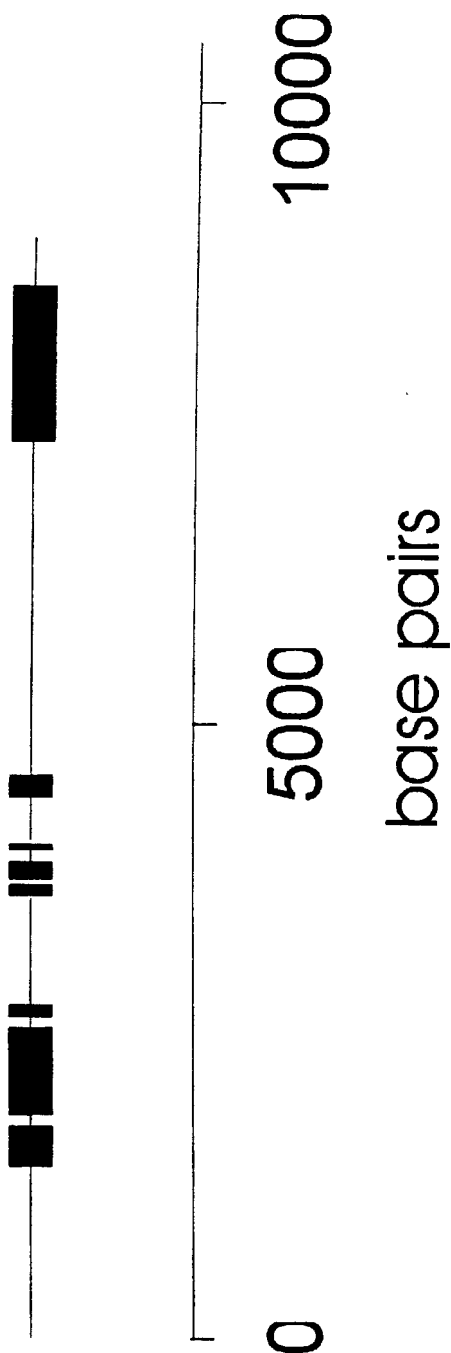


FIGURE 6

1001701

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3001841

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| |
|-----------|
| FIGURE 7A |
| FIGURE 7B |
| FIGURE 7C |
| FIGURE 7D |
| FIGURE 7E |
| FIGURE 7F |
| FIGURE 7G |
| FIGURE 7H |
| FIGURE 7I |

FIGURE 7

1 MEMSLWPRSP LCPRSRQPLV VVRP..AGRG GLTQPFLMNG RFTRSRTRLRC 50
MEMVLRSQSP LCLRS.GPVL IFRPTVAGGG GGTQSLRRT RFARRRVIRC
pSSIII ~~~~~
51 MVASSDPPNR KSRMVPPQV KVISSRGYTT RLIVEPSNEN TEHNNRD... 100
VVASPGCPNR KS.RTASPNV KVAAYSNYAP RLLVESSSKK SEHHDSSRHR
pSSIII ~~~~~
101 EETLDTYNAL LSTETAETD NRAE..... ..TAKADSSQ NALSSSIIGE 150
EETIDTYNGL SGSDAAELTS NRDVEIEVDL QHISEEELPG KVSINASLGE
pSSIII ~~~~~
151 VDVAD..... EDILAADLTV YSLSSVMKKE VDAADKARVK EDAFELDLP 200
METVDEAEVE EDKFEVDTSI IVLRNVAVRE VDPKDEHNAK .DVFVVDSSG
pSSIII ~~~~~

FIGURE 7A

| | | | | | |
|--------|------------|------------|------------|-------------|------------|
| 201 | 250 | | | | |
| wSSIII | TLRSVIVDV | MDHNGTVQET | LRSVIVDVM | :HNGTVQE.. | TLRSVIVDVM |
| mSSIII | TAPDNAAVEE | VVDEAEVEED | MVDVDILGLD | LNNATIEEID | LMEEALLENF |
| pSSIII | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~ |
| 251 | 300 | | | | |
| wSSIII | D.DAADKARV | EEDVFELDLS | GNISSAT.. | | TVEL |
| mSSIII | DVDSPGNASS | GRTYGGVDEL | GELPSTSVDC | IAINGKRRSL | KPKPLPIVRF |
| pSSIII | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~ |
| 301 | 350 | | | | |
| wSSIII | DAVDEVGPVQ | DKFEATSSGN | VNSATVREV | DASDE...AG | NDQGIFRADL |
| mSSIII | QEQEQIVLSI | VDEEGLIASS | CEEGQPVVDY | DKQEEENSTAF | DEQKQLTDDF |
| pSSIII | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~ |
| 351 | 400 | | | | |
| wSSIII | SGNVFSSSTT | VEVG..AVDE | AGSIKDRFET | DSSGNVSTSA | PMWDAIDETV |
| mSSIII | PEEGISIVHF | PEPNNDIVGS | SKFLEKQKEL | DGSYKQDRST | TGLHEQDQSV |
| pSSIII | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~ |

FIGURE 7B

| | | | | | |
|--------|--------------|-------------|-------------|-------------|--------------|
| wSSIII | ADQDTFEADL | SGNASSCATY | REVDDVVDET | RSEETTFAMD | LFAESGHEK |
| mSSIII | VSSHGQDKSI | VG.VPQQIQY | NDQSIAGSHR | QDQSIAGAPE | QIQSVAGYIK |
| pSSIII | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~~ | ~~~~MDVPF |
| | 401 | | | | 450 |
| wSSIII | HMAVDYVGEA | TDEEETYQQQ | YPVPSSFMMW | DKAIAKTGVS | LNPELRLLVRV |
| mSSIII | PNQ.SIVGSC | KQHელიIPEP | KKIESII SYN | EIDQSI VGSH | KQDKSVVSVVP |
| pSSIII | PLHRSLSCTS | VSNAITHLKI | KPILGFVSHG | TTSLSVQSSS | WRKDGMVTGV |
| | 451 | | | | 500 |
| wSSIII | EEQGKVNFSD | KKDLSIDDL P | GQNQSIIGSY | KQDKSIADVA | GPTQSI FGSS |
| mSSIII | EQIQSIVSHS | KPNQSTVDSY | RQAESIIGVP | EKVQSITSYD | KLDQSI VGS L |
| pSSIII | SFSICANFSG | RRRRKVSTPR | SQSSSPKGFV | PRKP SGMSTQ | RKVQKSNGDK |
| | 501 | | | | 550 |
| wSSIII | KQHR SIVA FP | KQNQ SIVSVT | EQKQ SIVGFR | SQDLSAVSL. | P |
| mSSIII | KQDEPIISVP | EKI QSIVHYT | KPNQ SIVGLP | KQQQ SIVHIV | EPKQ SIDGFP |
| pSSIII | ESKSTSTSKE | SEISNQKTVE | ARVETSDDDT | KGVRDHKFL | EDEDEINGST |
| | 551 | | | | 600 |

FIGURE 7C

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| | | |
|--------|---|-----|
| 601 | | 650 |
| wSSIII | KQ.NVPIVGT SREGQTKQVP VVDRQDALYV NGLEAKEGDH TSEKTD DAL | |
| mSSIII | KQ.DLSIVGI SNEFQTKQLA TVGTHDGLLM KGVEAKE... TSQKTEGDTL | |
| pSSIII | KSISMSPPRV SSQFVESEET GGDDKDAVKL N..KSKRSEE SGFIIDSVIR | |
| 651 | | 700 |
| wSSIII | HVKFNVDNVL RKHQADRTQA VEKKTWKKVD EEHLYMTEHQ KRAA..EGQM | |
| mSSIII | QATFNVDNLS QKQEGLTKEA DEITIIIEKIN DEDLVMIEEQ KSIAMNEEQ | |
| pSSIII | EQSGSQGETN ASSKGSHAVG TKLYEILQVD VEPQQLEN. .NAGNVEYKG | |
| 701 | | 750 |
| wSSIII | VVNEDELSIT EIGMGRGD.K IQHVLSEEL SWSEDEVQLI EDDGQYEVDE | |
| mSSIII | IVTEEDIPMA KVEIGIDKAK FLHLLSEES SWDENEVGII EADEQYEVDE | |
| pSSIII | PVASKLLEIT KA.....SD VEHTESNEID DLDN..SFF KSDLIEEDEP | |
| 751 | | 800 |
| wSSIII | TSVSVNVEQD IQGSPQDVVD PQALKVMLQE LAEKNYSMRN KLFVFFPEVVK | |
| mSSIII | TSMS..TEQD IQESPNDLD PQALWSMLQE LAEKNYSLGN KLFTYPPDVLK | |
| pSSIII | LAAGTVETGD SSLNLRLEME ANLRRQAIER LAEENLLQGI RLFCFPEVVK | |

FIGURE 7D

| | | | | | | |
|--------|------------|-------------|------------|------------|-------------|------|
| 801 | ADSVIDLVLN | RDLTALANEP | DVVIKGAENG | WKWRLFTERL | HKSDLGGVWW | 850 |
| wSSIII | ADSTIDLVLN | RDLTALANEP | DVVIKGAENG | WKWRLFTERL | HKSDLGGVWW | |
| mSSIII | PDEDVEIFLN | RGLSTLKNES | DVLIMGAFNE | WRYRSFTTRL | TETHLNGDWW | |
| pSSIII | | | | | | |
| 851 | SCKLYIPKEA | YRLDFVFFNG | RTVYENNGNN | DFCIGIEGTM | NEDLFEDFLV | 900 |
| wSSIII | CCKLYIPKQA | YRMDVFFNG | HTVYENNNNN | DFVIQIESTM | DENLFEDFLA | |
| mSSIII | SCKIHVPKEA | YRADFVFFNG | QDVYDNNDGN | DFSITVKGGM | QIIDFENFLL | |
| pSSIII | | | | | | |
| 901 | KEKQRELEKL | AMEEAERRTQ | TEEQRRRKEA | RAADEAVRAQ | AKAEIEIKKK | 950 |
| wSSIII | EEKQRELENL | ANEEAERRRQ | TDEQRRMEEE | RAADKADRVQ | AKVEVETKKN | |
| mSSIII | EEKWREQEKL | AKEQAEERERL | AAEQRRIEAE | KAEIEADRAQ | AKEEAACKKK | |
| pSSIII | | | | | | |
| 951 | KLQSMLSLAR | TCVDNLWYIE | ASTDTRGDTI | RLYYNRNSRP | LAHSTEIWMH | 1000 |
| wSSIII | KLCNVLGLAR | APVDNLWYIE | PITGQEATV | RLYYNINSRP | LVBHSTEIWMH | |
| mSSIII | VLRELMVKAT | KTRDITWYIE | PSEFKCEDKV | RLYYNKSSGP | LSHAKDLWIH | |
| pSSIII | | | | | | |

FIGURE 7E

| | | | | | | |
|--------|------------|------------|-------------|-------------|------------|------|
| 1001 | GGYNNWTDGL | SIVESFVKCN | DKDGDWWYAD | VIPPEKALVL | DWVFADGPAG | 1050 |
| wSSIII | | | | | | |
| mSSIII | GGYNNWIDGL | SFAERLVHHH | DKDCDWWFAD | VVVPERTYVL | DWVFADGPPG | |
| pSSIII | GGYNNWKDGL | SIVKKLVKSE | RIDGDWWYTE | VVIPDQALFL | DWVFADGPPK | |
| 1051 | NARNYDNNAR | QDFHAILPNN | NVTEEGFWAQ | EEQNIYTRLL | QERREKEETM | 1100 |
| wSSIII | | | | | | |
| mSSIII | SARNYDNNGG | HDFHATLP.N | NMTTEEEYWME | EEQRIYTRLQ | QERREREEAI | |
| pSSIII | HAIAYDNNHR | QDFHAIVP.N | HIPEELYWVE | EEHQIFKTLQ | EERLREAAM | |
| 1101 | KRKAERSANI | KAEMKAKTMR | RFLSQKHIV | YTEPLEIRAG | TTVDVLYNPS | 1150 |
| wSSIII | | | | | | |
| mSSIII | KRKAERNAKM | KAEMKEKTMR | MFLVSQKHIV | YTEPLEIHAG | TTIDVLYNPS | |
| pSSIII | RAKVEKTALL | KTETKERTMK | SFLSQKHVV | YTEPLDIQAG | SSVTVYYNPA | |
| 1151 | NTVLNGKSEG | WFRCSFNLWM | HSSGALPPQK | MVKSGDGP LL | KATVDVPPDA | 1200 |
| wSSIII | | | | | | |
| mSSIII | NTVLTGKPEV | WFRCSFNRWM | YPGGVLPQK | MVQAENGSHL | KATVYVPRDA | |
| pSSIII | NTVLNGKPEI | WFRCSFNRWT | HRGLPLPPQK | MSPAENGTHV | RATVKVPLDA | |

FIGURE 7F

| | | | | | | | |
|------|--------|-------------|------------|------------|------------|------------|------|
| 1201 | wSSIII | YMMDFVFSEW | EEDGIYDNRN | GMDYHIPVSD | SIETENYMRI | IHIAVEMAPV | 1250 |
| | mSSIII | YMMDFVFSES | EEGGIYDNRN | GLDYHIPVFG | SIAKEPPMHI | VHIAVEMAPI | |
| | pSSIII | YMMDFVFSEW | EDGGIFDNKS | GMDYHIPVFG | GVAKEPPMHI | VHIAVEMAPI | |
| 1251 | wSSIII | AKVGGGLGDVV | TSLSRAIQDL | GHTVEVILPK | YDCLNQSSVK | DLHLYQSFWS | 1300 |
| | mSSIII | AKVGGGLGDVV | TSLSRAVQDL | GHNVEVILPK | YGCLNLSNVK | NLQIHQSFWS | |
| | pSSIII | AKVGGGLGDVV | TSLSRAVQDL | NHNVDIILPK | YDCLKMNNVK | DFRFHKNYFW | |
| 1301 | wSSIII | GGTEIKVWVG | RVEDLTVYFL | EPQNGMFGVG | CVYG.RNDDR | RFGFFCHSAL | 1350 |
| | mSSIII | GGSEINVWRG | LVEGLCVYFL | EPQNGMFGVG | YVYG.RDDDR | RFGFFCRSAL | |
| | pSSIII | GGTEIKVWFG | KVEGLSVYFL | EPQNGLFSKG | CVYGCSNDGE | RFGFFCHAAL | |
| 1351 | wSSIII | EFILQNEFSP | HIHCHDWSS | APVAWLKHEH | YSQSRMASTR | VVFTIHNLEF | 1400 |
| | mSSIII | EFLQSGSSP | NIIHCHDWSS | APVAWLHKEN | YAKSSLANAR | VVFTIHNLEF | |
| | pSSIII | EFLQGGFSP | DIIHCHDWSS | APVAWLFKEQ | YTHYGLSKSR | IVFTIHNLEF | |

FIGURE 7G

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| | | | | | | |
|--------|------------|------------|------------|-------------|-------------|------|
| 1401 | GAHYIGKAMT | YCDKATTVSP | TYSRDVAGHG | AIAPHREKFY | GILNGIDPDI | 1450 |
| wSSIII | | | | | | |
| mSSIII | GAHHIGKAMR | YCDKATTVSN | TYSKEVSGHG | AIVPHLGKFY | GILNGIDPDI | |
| pSSIII | GADLIGRAMT | NADKATTVSP | TYSQEVSGNP | VIAPHLHKFH | GIVNGIDPDI | |
| 1451 | WDPYTDNFIP | VPYTCENVVE | GKRAAKRALQ | QKFGGLQQTDV | PIVGIIITRLT | 1500 |
| wSSIII | | | | | | |
| mSSIII | WDPYNDNFIP | VHYTCENVVE | GKRAAKRALQ | QKFGGLQQIDV | PVVGIVITRLT | |
| pSSIII | WDPLNDKFIP | IPYTSENVVE | GKTAAKEALQ | RKLGLKQADL | PLVGIIITRLT | |
| 1501 | AQKGIHLIKH | AIHRTLESNG | HVVLLGSAPD | HRIQGDFCRL | ADALHGVYHG | 1550 |
| wSSIII | | | | | | |
| mSSIII | AQKGIHLIKH | AIHRTLERNG | QVVLLGSAPD | SRIQADFVNL | ANTLHGVNHG | |
| pSSIII | HQKGIHLIKH | AIWRTLERNG | QVVLLGSAPD | PRVQNNFVNL | ANQLHSKYND | |
| 1551 | RVKLVLTIDE | PLSHLIYAGS | DFIIVPSIFE | PCGLTQLVAM | RYGSIPIVRK | 1600 |
| wSSIII | | | | | | |
| mSSIII | QVRLSLTYDE | PLSHLIYAGS | DFILVPSIFE | PCGLTQLVAM | RYGTIPIVRK | |
| pSSIII | RARLCLTYDE | PLSHLIYAGA | DFILVPSIFE | PCGLTQLTAM | RYGSIPIVVRK | |

FIGURE 7H

Title: Genes Encoding Wheat Starch Synthases
and Uses Therefor

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Inventors: Morrell et al.

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Filing Date: October 29, 2001

| | | | | | |
|--------|------------|------------|------------|------------|------------|
| 1601 | 1650 | | | | |
| wSSIII | TGGLHDTVFD | VDNDKDRARS | LGLEPNGFSF | DGADSNQVDY | ALNRAIGAWF |
| mSSIII | TGGLFDTVFD | VDNDKERARD | RGLEPNGFSF | DGADSNQVDY | ALNRAISAWF |
| pSSIII | TGGLYDTVFD | VDHDKERAQQ | CGLEPNGFSF | DGADAGGVDY | ALNRALSAWY |
| 1651 | 1689 | | | | |
| wSSIII | DARDWFHSLC | KRVMEQDWSW | NRPALDYIEL | YHAARKF* | |
| mSSIII | DARSWFHSLC | KRVMEQDWSW | NRPALDYIEL | YRSASKL~ | |
| pSSIII | DGRDWFNSLC | KQVMEQDWSW | NRPALDYIEL | YHAARKLE* | |

FIGURE 7I

Title: Genes Encoding Wheat Starch Synthases

and Uses Therefor

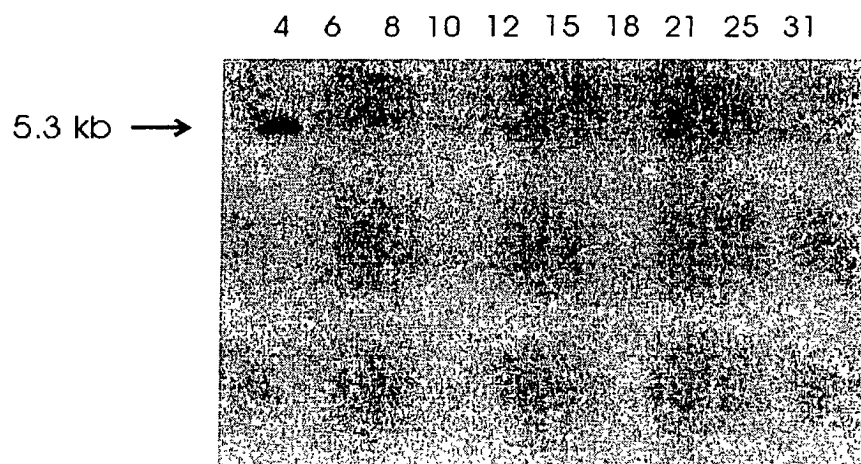
Inventors: Morrell et al.

Filing Date: October 29, 2001

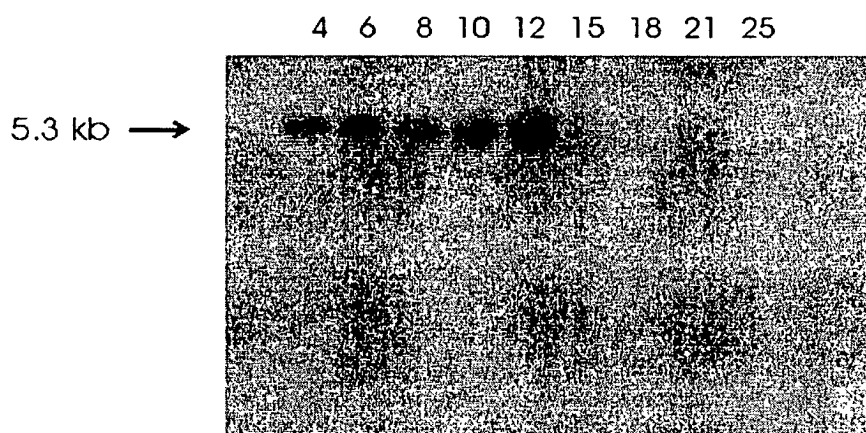
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[a] Wyuna



[b] Gabo



[c] Gabo



FIGURE 8

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| | |
|-----------|-----------|
| FIGURE 9A | FIGURE 9B |
| FIGURE 9C | FIGURE 9D |
| FIGURE 9E | FIGURE 9F |

FIGURE 9

FIGURE 9A

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Inventors: Morrell et al.

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| | | | | |
|-------------|------------|------------|------------|------|
| 60 | 70 | 80 | 90 | |
| -----SVVSE | IKVVDKYERV | RYFHCYKRGV | DRVFDHPCF | 170 |
| KALYTGKHIK | *PCFGGSHE* | TF**E*RDN* | *W*****SY | 233 |
| -----G*RKY | Y*AAQDME* | N***A*ID** | *F**I*A*L* | 403 |
| ----- | -DLHLYQSFS | WGGTEI*VW* | G**EDLTVY* | 1276 |
| | | | | |
| 150 | 160 | 170 | 180 | |
| SGPYGEDVVF | VCNDWHTGLL | ACYLKSNIQS | NGIYRAAKVA | 260 |
| QN-----CM* | *V***AS*V | PVL*AAK*RP | Y*V**DSRST | 323 |
| D*-----NL** | IA*****A** | PV***AY*RD | H*LMQYTRSI | 493 |
| -----II | H*H**SSAPV | *WLY*EH*SQ | -SRMASTR*V | 1366 |
| | | | | |
| 240 | 250 | 260 | 270 | |
| NWMKAGILQA | DKVLTVSPYY | AEELISGEAR | GCELDNIMRL | 350 |
| FLKG*VVTAD | RI*TVSQG*S | W*VTTAEGGQ | *LNELLSS*K | 413 |
| YFAAGLKMAD | QV*VVSPG*L | W*LKTVEGGW | *LHDIIRQND | 583 |
| ----- | -----AT | TVSPTYSRDV | AGHGAIAPHR | 1456 |

FIGURE 9B

Region 4

| | | | | | |
|-------|------|-----------------------|------------|-------------|------------|
| | 280 | 290 | 300 | 310 | 320 |
| wGBSS | 351 | TGITTIVNGM DVSEWDPTKD | KFLAVNYDIT | TALEGKALNK | EALEGKALNK |
| wSS1 | 414 | SVLNG***I *IND*N**T* | *C*PHH*SV- | ----- | DD*S**KC* |
| wSS2 | 584 | WKTRG***I *NM**N*EV* | VH*KSDGYTN | -----FSLG | TLDS**RQC* |
| wSS3 | 1457 | EKFYGL**I *PDI***YT* | N*IP*P*TCE | -----NVVEG* | **AKRALQQ* |

Region 5a

| | | | | | |
|-------|------|-----------------------|------------|------------|------------|
| | 370 | 380 | 390 | 400 | 410 |
| wGBSS | 441 | LKEEDVQIVL LGTGKKKFER | LLKSIEEKFP | SKVRVVREN | -----APLA |
| wSS1 | 504 | *MR***F*M **S*DPI**G | WMR*T*SSYK | D*F*GW*G*S | -----V*VS |
| wSS2 | 674 | V-SQ***L*M ***RHDLS | M*RHF*REHH | D**GW*G*S | -----VR** |
| wSS3 | 1547 | TL*SNG*V** **SAPDHRIQ | GDFCRLADAL | HG*YHGRVKL | -VLTIDE**S |

FIGURE 9C

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| | | | |
|------------|------------|-------------|------------------|
| Region 5 | | | |
| 330 | 340 | 350 | 360 |
| EALQAEVGLP | VDRKVPLVAF | IGRLEEQKGP | DVMIASIP EI |
| AE**K*L** | *RED***IG* | *****DY***I | *LIKMA***- |
| ***R*L**Q | *RAD***LG* | *****DG***V | EIIADAM*W* |
| FG**QT---- | ---D**I*GI | *T**TA***I | -HL*KHAIHR |
| | | | 440 503 673 1546 |
| Region 6 | | Region 7 | |
| 420 | 430 | 440 | 450 |
| HQMMAGADVL | AVTSRFEPCG | LIQLQGMRYG | TPCACASTGG |
| *RIT**C*I* | LMP***** | *N**YA*Q** | *VPVVG*** |
| *RIT***A* | LMP***** | *N**YA*A** | *VPVHVAV** |
| *LIY**S*FI | I*P*I***** | *T**VA*** | SIPIVRK*** |
| | | | 530 593 763 1636 |

FIGURE 9D

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Region 7 (Continued)

| | 460 | 470 | 480 | 490 | 500 |
|-----------|---------------|------------|------------|------------|------------|
| wGBSS 531 | LVDTIVEGKT | GFHMGRLSYD | CNVVEPADVK | KVVTTLKRAV | KVVGTPAYHE |
| wSS1 594 | *R**--**TFN | ----- | --PFGAKGEE | GTGWAFSPLT | VDKMLW*LRT |
| wSS2 764 | VR**--*PPFD | ----- | --PFNHSGLG | --W*FD**E | AHKLIE*LGH |
| wSS3 1637 | ***--*FDV | NDKDRAR*LG | LEPNGFSFDG | ADSNGVGY*L | NRAIGAWFDA |
| 550 | 560 | 570 | 580 | 590 | 600 |
| wGBSS 621 | APLAMENVAA P* | | | | |
| wSS1 684 | FVDQPYVM.. | | | | |
| wSS2 854 | KYQW..... | | | | |
| wSS3 1727 | | | | | |

FIGURE 9E

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| | | | | | |
|-----|------------|------------|------------|------------|------|
| 510 | MVKNCMIQDL | SWKGPAKNWE | DVLELGVEG | SEPGIVGEEI | 620 |
| | AMSTFEHKE | **E*LM*RG | TKDHTWDHAA | EQYEQIF*WA | 683 |
| | CLRTYRDYKE | **R*LQERGM | SQDFSWEHAA | KLYED*LLKA | 853 |
| | RDWFHSLCKK | VMEQDWSWNR | PA*DYIELYH | AARKF*.... | 1726 |
| 610 | | 620 | 630 | | |
| | | | | | 710 |
| | | | | | 773 |
| | | | | | 943 |
| | | | | | 1816 |

FIGURE 9F

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4/1/00

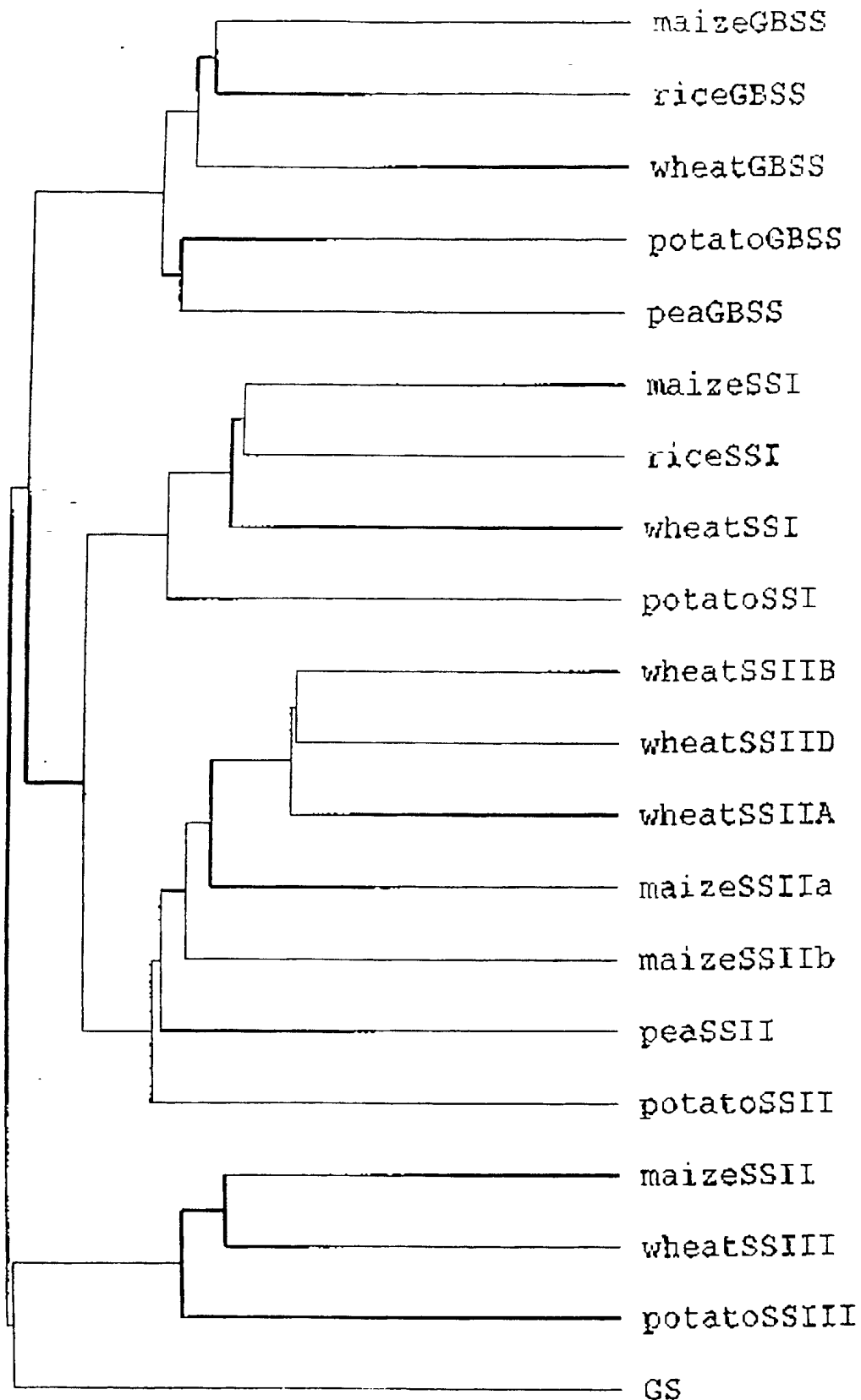


FIGURE 10

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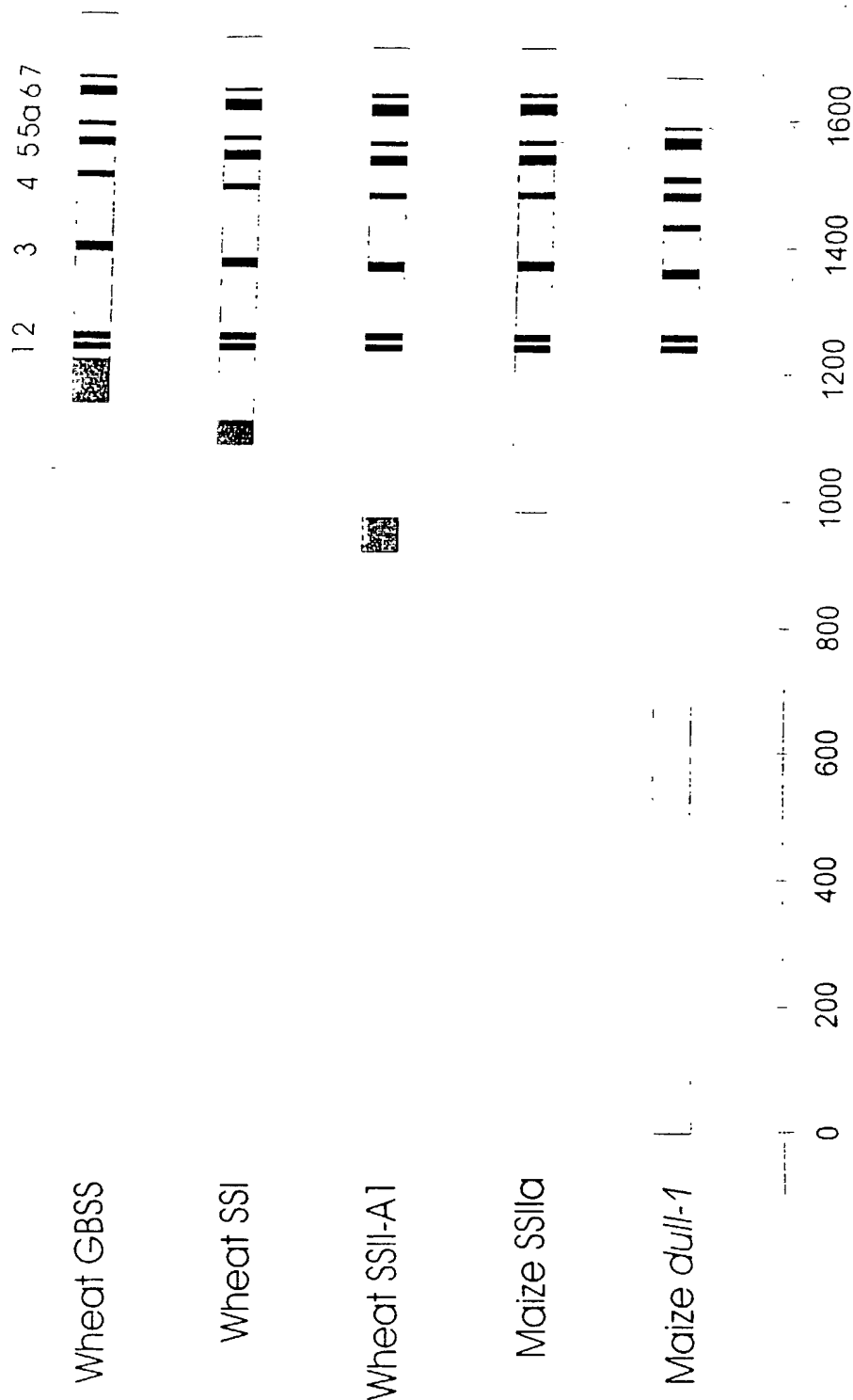


FIGURE 11

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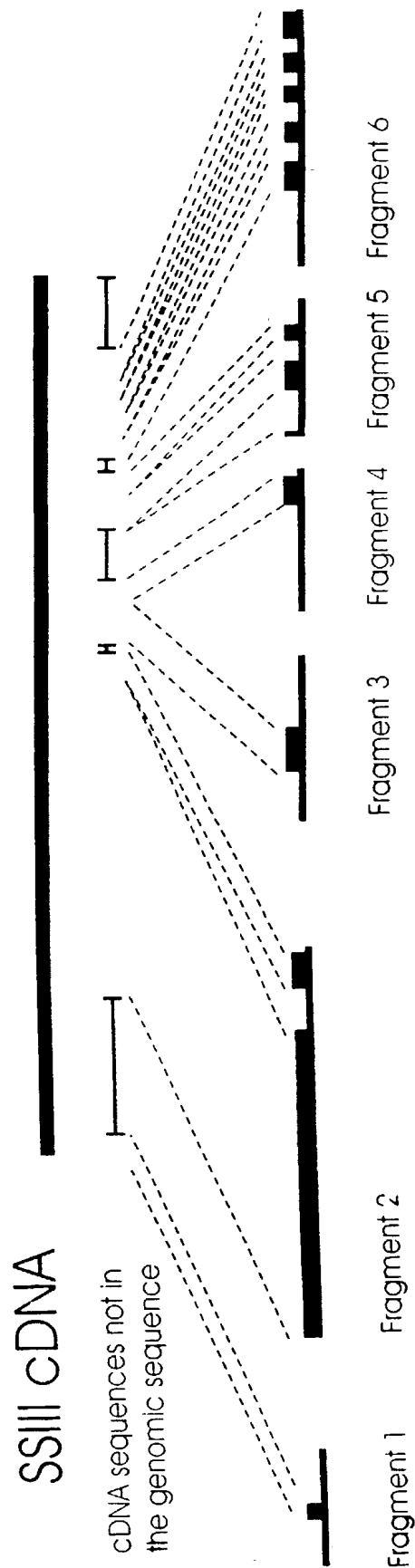


FIGURE 12

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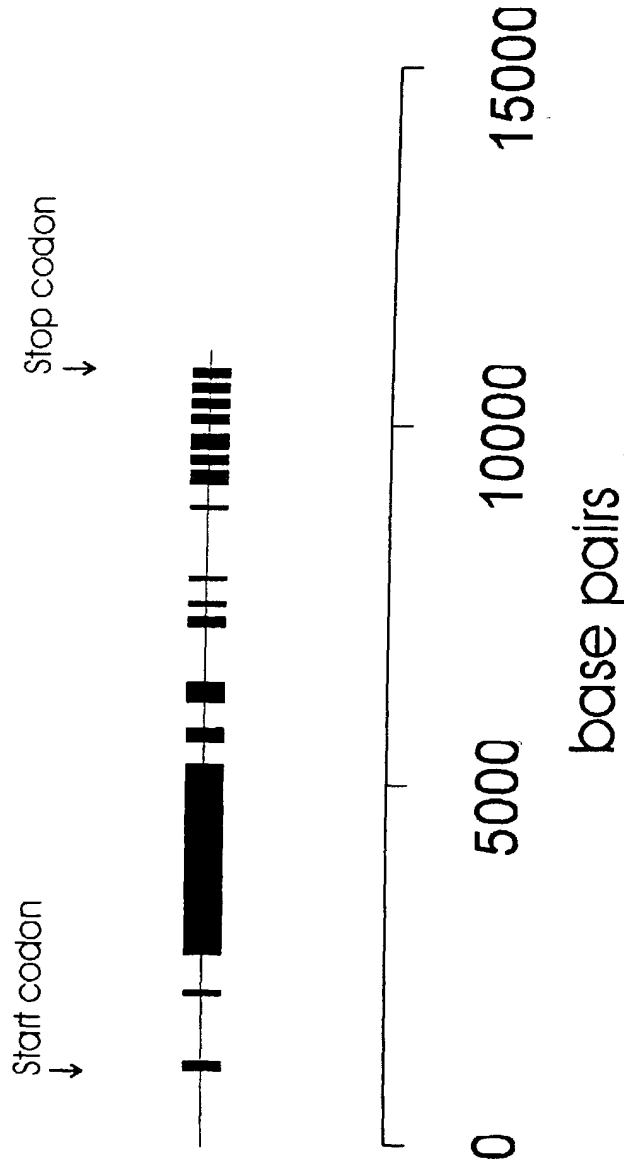
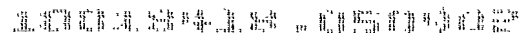


FIGURE 13



As the below named inventors, we hereby declare that:

We believe that we are the original, first and joint inventors of the subject matter which is claimed and for which a patent is sought on the invention entitled:

the specification of which was filed on 28 April 2000 as PCT/AU00/00385 and was amended on 29 October, 2001.

We acknowledge the duty to disclose information which is material to the patentability of this application in accordance with Title 37, Code of Federal Regulations, §1.56.

We hereby claim foreign priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application(s) for patent or inventor's certificate having a filing date before that of the application to which priority is claimed:

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[illegible]

5

Date of Filing
(day,month,year)

Status(Patented,Pending,Abandoned)

10

We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

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400

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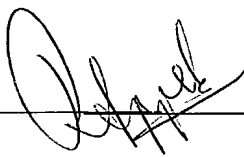
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Australia

67c. Gardner St

Cornog, Perth, Western Australia
6151

(4) Signature

x 

Date

x 21/01/02

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SEQUENCE LISTING

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 GOODMAN FIELDER LIMITED
 GROUPE LIMAGRAIN PACIFIC PTY LTD

<120> NOVEL GENES ENCODING WHEAT STARCH SYNTHASES AND USES
 THEREFOR

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<140> TO BE ADVISED

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<150> AU PQ0052/99

<151> 1999-04-29

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 Ala Gly Ile Asp Asp Ala Ala Pro Ala Arg Gln Pro Arg Ala Leu Arg
 70 75 80

ggc ggc gcc gcc acc aag gtt gcg gag ccg agg gat ccc gtc aag acg 466
 Gly Gly Ala Ala Thr Lys Val Ala Glu Arg Arg Asp Pro Val Lys Thr
 85 90 95

ctc gat cgc gac gcc gcg gaa ggt ggc gcg ccg tcc ccg ccg gca ccg 514
 Leu Asp Arg Asp Ala Ala Glu Gly Gly Ala Pro Ser Pro Pro Ala Pro

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| | | | |
|---|-----|-----|------|
| 100 | 105 | 110 | |
| agg cag gag gac gcc cgt ctg ccg agc atg aac ggc atg ccg gtg aac | | | 562 |
| Arg Gln Glu Asp Ala Arg Leu Pro Ser Met Asn Gly Met Pro Val Asn | | | |
| 115 | 120 | 125 | |
| ggt gaa aac aaa tct acc ggc ggc ggc ggc gcg act aaa gac agc ggg | | | 610 |
| Gly Glu Asn Lys Ser Thr Gly Gly Gly Gly Ala Thr Lys Asp Ser Gly | | | |
| 130 | 135 | 140 | 145 |
| ctg ccc gca ccc gca cgc gcg ccc cag ccg tcg agc cag aac aga gta | | | 658 |
| Leu Pro Ala Pro Ala Arg Ala Pro Gln Pro Ser Ser Gln Asn Arg Val | | | |
| | 150 | 155 | 160 |
| ccg gtg aat ggt gaa aac aaa gct aac gtc gcc tcg ccg ccg acg agc | | | 706 |
| Pro Val Asn Gly Glu Asn Lys Ala Asn Val Ala Ser Pro Pro Thr Ser | | | |
| | 165 | 170 | 175 |
| ata gcc gag gtc gcg gct ccg gat ccc gca gct acc att tcc atc agt | | | 754 |
| Ile Ala Glu Val Ala Ala Pro Asp Pro Ala Ala Thr Ile Ser Ile Ser | | | |
| | 180 | 185 | 190 |
| gac aag gcg cca gag tcc gtt gtc cca gcc gag aag gcg ccg ccg tcg | | | 802 |
| Asp Lys Ala Pro Glu Ser Val Val Pro Ala Glu Lys Ala Pro Pro Ser | | | |
| | 195 | 200 | 205 |
| tcc ggc tca aat ttc gtg ccc tcg gct tct gct ccc ggg tct gac act | | | 850 |
| Ser Gly Ser Asn Phe Val Pro Ser Ala Ser Ala Pro Gly Ser Asp Thr | | | |
| 210 | 215 | 220 | 225 |
| gtc agc gac gtg gaa ctt gaa ctg aag aag ggt gcg gtc att gtc aaa | | | 898 |
| Val Ser Asp Val Glu Leu Glu Leu Lys Lys Gly Ala Val Ile Val Lys | | | |
| | 230 | 235 | 240 |
| gaa gct cca aac cca aag gct ctt tcg ccg ccc gca gca ccc gct gta | | | 946 |
| Glu Ala Pro Asn Pro Lys Ala Leu Ser Pro Pro Ala Ala Pro Ala Val | | | |
| | 245 | 250 | 255 |
| caa caa gac ctt tgg gac ttc aag aaa tac att ggt ttc gag gag ccc | | | 994 |
| Gln Gln Asp Leu Trp Asp Phe Lys Lys Tyr Ile Gly Phe Glu Glu Pro | | | |
| | 260 | 265 | 270 |
| gtg gag gcc aag gat gat ggc cgg gct gtt gca gat gat gcg ggc tcc | | | 1042 |
| Val Glu Ala Lys Asp Asp Gly Arg Ala Val Ala Asp Asp Ala Gly Ser | | | |
| | 275 | 280 | 285 |
| ttc gaa cac cac cag aat cac gat tcc ggg cct ttg gca ggg gag aac | | | 1090 |
| Phe Glu His His Gln Asn His Asp Ser Gly Pro Leu Ala Gly Glu Asn | | | |
| 290 | 295 | 300 | 305 |
| gtc atg aac gtg gtc gtc gtg gct gct gaa tgt tct ccc tgg tgc aaa | | | 1138 |
| Val Met Asn Val Val Val Val Ala Ala Glu Cys Ser Pro Trp Cys Lys | | | |
| | 310 | 315 | 320 |
| aca ggt ggt ctt gga gat gtt gcc ggt gct ttg ccc aag gct ttg gcg | | | 1186 |
| Thr Gly Gly Leu Gly Asp Val Ala Gly Ala Leu Pro Lys Ala Leu Ala | | | |
| | 325 | 330 | 335 |
| aag aga gga cat cgt gtt atg gtt gtg gta cca agg tat ggg gac tat | | | 1234 |
| Lys Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr Gly Asp Tyr | | | |
| | 340 | 345 | 350 |
| gag gaa gcc tac gat gtc gga gtc cga aaa tac tac aag gct gct gga | | | 1282 |
| Glu Glu Ala Tyr Asp Val Val Val Arg Lys Tyr Tyr Lys Ala Ala Gly | | | |
| | 355 | 360 | 365 |

| | | | | | | | | | | | | | | | | |
|-------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| cag Gln 370 | gat Asp | atg Met | gaa Glu | gtg Val | aat Asn | tat Tyr | ttc Phe | cat His | gct Ala | tat Tyr | atc Ile | gat Asp | gga Gly | gtt Val | gat Asp | 1330 |
| ttt Phe | gtg Val | ttc Phe | att Ile | gac Asp | gct Ala | cct Pro | ctc Leu | ttc Phe | cga Arg | cac His | cgc Arg | cag Gln | gaa Glu | gac Asp | att Ile | 1378 |
| tat Tyr | ggg Gly | ggc Gly | agc Ser | aga Arg | cag Gln | gaa Glu | att Ile | atg Met | aag Lys | cgc Arg | atg Met | att Ile | ttg Leu | ttc Phe | tgc Cys | 1426 |
| aag Lys | gcc Ala | gct Ala | gtc Val | gag Glu | gtt Val | cca Pro | tgg Trp | cac His | gtt Val | cca Pro | tgc Cys | ggc Gly | ggt Gly | gtc Val | cct Pro | 1474 |
| tat Tyr | ggg Gly | gat Asp | gga Gly | aat Asn | ctg Leu | gtg Val | ttt Phe | att Ile | gca Ala | aat Asn | gat Asp | tgg Trp | cac His | acg Thr | gca Ala | 1522 |
| ctc Leu | ctg Leu | cct Pro | gtc Val | tat Tyr | ctg Leu | aaa Lys | gca Ala | tat Tyr | tac Tyr | agg Arg | gac Asp | cat His | ggt Gly | ttg Leu | atg Met | 1570 |
| cag Gln | tac Tyr | act Thr | cgg Arg | tcc Ser | att Ile | atg Met | gtg Val | ata Ile | cat His | aac Asn | atc Ile | gct Ala | cac His | cag Gln | ggc Gly | 1618 |
| cgt Arg | ggc Gly | cca Pro | gta Val | gat Asp | gag Glu | ttc Phe | ccg Pro | ttc Phe | acc Thr | gag Glu | ttg Leu | cct Pro | gag Glu | cac His | tac Tyr | 1666 |
| ctg Leu | gaa Glu | cac His | ttc Phe | aga Arg | ctg Leu | tac Tyr | gac Asp | ccc Pro | gtg Val | ggt Gly | ggt Gly | gaa Glu | cac His | gcc Ala | aac Asn | 1714 |
| tac Tyr | ttc Phe | gcc Ala | gcc Ala | ggc Gly | ctg Leu | aag Lys | atg Met | gcg Ala | gac Asp | cag Gln | gtt Val | gtc Val | gtc Val | gtg Val | agc Ser | 1762 |
| ccg Pro | ggg Gly | tac Tyr | ctg Leu | tgg Trp | gag Glu | ctg Leu | aag Lys | acg Thr | gtg Val | gag Glu | ggc Gly | ggc Gly | tgg Trp | ggg Gly | ctt Leu | 1810 |
| cac His | gac Asp | atc Ile | ata Ile | cgg Arg | cag Gln | aac Asn | gac Asp | tgg Trp | aag Lys | acc Thr | cgc Arg | ggc Gly | atc Ile | gtg Val | aac Asn | 1858 |
| ggc Gly | atc Ile | gac Asp | aac Asn | atg Met | gag Glu | tgg Trp | aac Asn | ccc Pro | gag Glu | gtg Val | gac Asp | gtc Val | cac His | ctc Leu | aag Lys | 1906 |
| tcg Ser | gac Asp | ggc Gly | tac Tyr | acc Thr | aac Asn | ttc Phe | tcc Ser | ctg Leu | ggg Gly | acg Thr | ctg Leu | gac Asp | tcc Ser | ggc Gly | aag Lys | 1954 |
| cgg Arg | cag Gln | tgc Cys | aag Lys | gag Glu | gcc Ala | ctg Leu | cag Gln | cgg Arg | gag Glu | ctg Leu | ggc Gly | ctg Leu | cag Gln | gtc Val | cgc Arg | 2002 |
| ggc Gly | gac Asp | gtg Val | ccg Pro | ctg Leu | ctc Leu | ggc Gly | ttc Phe | atc Ile | ggg Gly | cgc Arg | ctg Leu | gac Asp | ggg Gly | cag Gln | aag Lys | 2050 |

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ggc gtg gag atc atc gcg gac gcg atg ccc tgg atc gtg agc cag gac 2098
Gly Val Glu Ile Ile Ala Asp Ala Met Pro Trp Ile Val Ser Gln Asp
630 635 640

gtg cag ctg gtc atg ctg ggc acc ggg cgc cac gac ctg gag ggc atg 2146
Val Gln Leu Val Met Leu Gly Thr Gly Arg His Asp Leu Glu Gly Met
645 650 655

ctg cgg cac ttc gag cgg gag cac cac gac aag gtg cgc ggg tgg gtg 2194
Leu Arg His Phe Glu Arg Glu His His Asp Lys Val Arg Gly Trp Val
660 665 670

ggg ttc tcc gtg cgg ctg gcg cac cgg atc acg gcc ggc gcc gac gcg 2242
Gly Phe Ser Val Arg Leu Ala His Arg Ile Thr Ala Gly Ala Asp Ala
675 680 685

ctc ctc atg ccc tcc cgg ttc gag ccg tgc gga ctg aac cag ctc tac 2290
Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln Leu Tyr
690 695 700 705

gcc atg gcc tac ggc acc gtc ccc gtc gtg cat gcc gtc ggt ggc ctg 2338
Ala Met Ala Tyr Gly Thr Val Pro Val Val His Ala Val Gly Gly Leu
710 715 720

agg gac acc gtg ccg ccg ttc gac ccc ttc aac cac tcc ggg ctc ggg 2386
Arg Asp Thr Val Pro Pro Phe Asp Pro Phe Asn His Ser Gly Leu Gly
725 730 735

tgg acg ttc gac cgc gca gag gcg cag aag ctg atc gag gcg ctc ggg 2434
Trp Thr Phe Asp Arg Ala Glu Ala Gln Lys Leu Ile Glu Ala Leu Gly
740 745 750

cac tgc ctc cgc acc tac cgg gac tac aag gag agc tgg agg ggg ctc 2482
His Cys Leu Arg Thr Tyr Arg Asp Tyr Lys Glu Ser Trp Arg Gly Leu
755 760 765

cag gag cgc ggc atg tcg cag gac ttc agc tgg gag cat gcc gcc aag 2530
Gln Glu Arg Gly Met Ser Gln Asp Phe Ser Trp Glu His Ala Ala Lys
770 775 780 785

ctc tac gag gac gtc ctc gtc aag gcc aag tac cag tgg tgaacgctag 2579
Leu Tyr Glu Asp Val Leu Val Lys Ala Lys Tyr Gln Trp
790 795

ctgctagccg gtccagcccc gcatgcgtgc atgacaggat ggaattgcgc attgcgcacg 2639

caggaagggtg ccatggagcg ccggcatccg cgaagtacag tgacatgagg tgtgtgtggt 2699

tgagacgctg attccgatct ggtccgtagc agagtagagc ggaggtaggg aagcgcctct 2759

tgttacaggt atatgggaat gttgttaact tggattgta atttgttatg ttgtgtgcat 2819

tattacagag ggcaacgata tgcgccggcg caccggccca actgttgggc cggtcgcaca 2879

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<211> 798
<212> PRT
<213> Triticum aestivum

<400> 2
Met Ser Ser Ala Val Ala Ser Ala Ala Ser Phe Leu Ala Leu Ala Ser
1 5 10 15

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- 5 -

Ala Ser Pro Gly Arg Ser Arg Arg Arg Thr Arg Val Ser Ala Ser Pro
20 25 30

Pro His Thr Gly Ala Gly Arg Leu His Trp Pro Pro Ser Pro Pro Gln
35 40 45

Arg Thr Ala Arg Asp Gly Ala Val Ala Ala Arg Ala Ala Gly Lys Lys
50 55 60

Asp Ala Gly Ile Asp Asp Ala Ala Pro Ala Arg Gln Pro Arg Ala Leu
65 70 75 80

Arg Gly Gly Ala Ala Thr Lys Val Ala Glu Arg Arg Asp Pro Val Lys
85 90 95

Thr Leu Asp Arg Asp Ala Ala Glu Gly Gly Ala Pro Ser Pro Pro Ala
100 105 110

Pro Arg Gln Glu Asp Ala Arg Leu Pro Ser Met Asn Gly Met Pro Val
115 120 125

Asn Gly Glu Asn Lys Ser Thr Gly Gly Gly Gly Ala Thr Lys Asp Ser
130 135 140

Gly Leu Pro Ala Pro Ala Arg Ala Pro Gln Pro Ser Ser Gln Asn Arg
145 150 155 160

Val Pro Val Asn Gly Glu Asn Lys Ala Asn Val Ala Ser Pro Pro Thr
165 170 175

Ser Ile Ala Glu Val Ala Ala Pro Asp Pro Ala Ala Thr Ile Ser Ile
180 185 190

Ser Asp Lys Ala Pro Glu Ser Val Val Pro Ala Glu Lys Ala Pro Pro
195 200 205

Ser Ser Gly Ser Asn Phe Val Pro Ser Ala Ser Ala Pro Gly Ser Asp
210 215 220

Thr Val Ser Asp Val Glu Leu Glu Leu Lys Lys Gly Ala Val Ile Val
225 230 235 240

Lys Glu Ala Pro Asn Pro Lys Ala Leu Ser Pro Pro Ala Ala Pro Ala
245 250 255

Val Gln Gln Asp Leu Trp Asp Phe Lys Lys Tyr Ile Gly Phe Glu Glu
260 265 270

Pro Val Glu Ala Lys Asp Asp Gly Arg Ala Val Ala Asp Asp Ala Gly
275 280 285

Ser Phe Glu His His Gln Asn His Asp Ser Gly Pro Leu Ala Gly Glu
290 295 300

Asn Val Met Asn Val Val Val Val Ala Ala Glu Cys Ser Pro Trp Cys
305 310 315 320

Lys Thr Gly Gly Leu Gly Asp Val Ala Gly Ala Leu Pro Lys Ala Leu
325 330 335

Ala Lys Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr Gly Asp
340 345 350

Tyr Glu Glu Ala Tyr Asp Val Gly Val Arg Lys Tyr Tyr Lys Ala Ala

| 355 | | | | | 360 | | | | | 365 | | | | | |
|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|-----|---------|
| Gly 370 | Gln | Asp | Met | Glu | Val | Asn 375 | Tyr | Phe | His | Ala | Tyr 380 | Ile | Asp | Gly | Val |
| Asp 385 | Phe | Val | Phe | Ile | Asp 390 | Ala | Pro | Leu | Phe | Arg 395 | His | Arg | Gln | Glu | Asp 400 |
| Ile | Tyr | Gly | Gly | Ser 405 | Arg | Gln | Glu | Ile | Met 410 | Lys | Arg | Met | Ile | Leu | Phe 415 |
| Cys | Lys | Ala | Ala | Val 420 | Glu | Val | Pro | Trp 425 | His | Val | Pro | Cys | Gly 430 | Gly | Val |
| Pro | Tyr | Gly 435 | Asp | Gly | Asn | Leu | Val 440 | Phe | Ile | Ala | Asn | Asp 445 | Trp | His | Thr |
| Ala 450 | Leu | Leu | Pro | Val | Tyr | Leu 455 | Lys | Ala | Tyr | Tyr | Arg 460 | Asp | His | Gly | Leu |
| Met 465 | Gln | Tyr | Thr | Arg | Ser 470 | Ile | Met | Val | Ile | His 475 | Asn | Ile | Ala | His | Gln 480 |
| Gly | Arg | Gly | Pro | Val 485 | Asp | Glu | Phe | Pro | Phe 490 | Thr | Glu | Leu | Pro | Glu | His 495 |
| Tyr | Leu | Glu | His 500 | Phe | Arg | Leu | Tyr | Asp 505 | Pro | Val | Gly | Gly | Glu 510 | His | Ala |
| Asn | Tyr | Phe 515 | Ala | Ala | Gly | Leu | Lys 520 | Met | Ala | Asp | Gln | Val 525 | Val | Val | Val |
| Ser 530 | Pro | Gly | Tyr | Leu | Trp | Glu 535 | Leu | Lys | Thr | Val | Glu 540 | Gly | Gly | Trp | Gly |
| Leu 545 | His | Asp | Ile | Ile | Arg 550 | Gln | Asn | Asp | Trp | Lys 555 | Thr | Arg | Gly | Ile | Val 560 |
| Asn | Gly | Ile | Asp | Asn 565 | Met | Glu | Trp | Asn | Pro 570 | Glu | Val | Asp | Val | His | Leu 575 |
| Lys | Ser | Asp | Gly 580 | Tyr | Thr | Asn | Phe | Ser 585 | Leu | Gly | Thr | Leu | Asp 590 | Ser | Gly |
| Lys | Arg | Gln 595 | Cys | Lys | Glu | Ala | Leu 600 | Gln | Arg | Glu | Leu | Gly 605 | Leu | Gln | Val |
| Arg | Gly 610 | Asp | Val | Pro | Leu | Leu 615 | Gly | Phe | Ile | Gly | Arg 620 | Leu | Asp | Gly | Gln |
| Lys 625 | Gly | Val | Glu | Ile | Ile 630 | Ala | Asp | Ala | Met | Pro 635 | Trp | Ile | Val | Ser | Gln 640 |
| Asp | Val | Gln | Leu | Val 645 | Met | Leu | Gly | Thr | Gly 650 | Arg | His | Asp | Leu | Glu | Gly 655 |
| Met | Leu | Arg | His 660 | Phe | Glu | Arg | Glu | His 665 | His | Asp | Lys | Val | Arg 670 | Gly | Trp |
| Val | Gly | Phe 675 | Ser | Val | Arg | Leu | Ala 680 | His | Arg | Ile | Thr | Ala 685 | Gly | Ala | Asp |
| Ala 690 | Leu | Leu | Met | Pro | Ser | Arg 695 | Phe | Glu | Pro | Cys | Gly 700 | Leu | Asn | Gln | Leu |

cca ccg agt atg aac ggc acg ccg gtg aac ggt gag aac aaa tct acc 496
Pro Pro Ser Met Asn Gly Thr Pro Val Asn Gly Glu Asn Lys Ser Thr

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|--|--|--|--|--|--|-----|--|--|--|--|--|
| | | | | | | | | | | 125 | | | | | | | 130 | | | | | | | 135 | | | | | |
| ggc | ggc | ggc | ggc | gcg | acc | aaa | gac | agc | ggg | ctg | ccc | gca | ccc | gca | cgc | 544 | | | | | | | | | | | | | |
| Gly | Gly | Gly | Gly | Ala | Thr | Lys | Asp | Ser | Gly | Leu | Pro | Ala | Pro | Ala | Arg | | | | | | | | | | | | | | |
| | | | 140 | | | | 145 | | | | | | 150 | | | | | | | | | | | | | | | | |
| gcg | ccc | cat | ccg | tcg | acc | cag | aac | aga | gta | cca | gtg | aac | ggt | gaa | aac | 592 | | | | | | | | | | | | | |
| Ala | Pro | His | Pro | Ser | Thr | Gln | Asn | Arg | Val | Pro | Val | Asn | Gly | Glu | Asn | | | | | | | | | | | | | | |
| | | | 155 | | | | 160 | | | | | | 165 | | | | | | | | | | | | | | | | |
| aaa | gct | aac | gtc | gcc | tcg | ccg | ccg | acg | agc | ata | gcc | gag | gtc | gtg | gct | 640 | | | | | | | | | | | | | |
| Lys | Ala | Asn | Val | Ala | Ser | Pro | Pro | Thr | Ser | Ile | Ala | Glu | Val | Val | Ala | | | | | | | | | | | | | | |
| | | | 170 | | | | 175 | | | | | | 180 | | | | | | | | | | | | | | | | |
| ccg | gat | tcc | gca | gct | acc | att | tcc | atc | agt | gac | aag | gcg | ccg | gag | tcc | 688 | | | | | | | | | | | | | |
| Pro | Asp | Ser | Ala | Ala | Thr | Ile | Ser | Ile | Ser | Asp | Lys | Ala | Pro | Glu | Ser | | | | | | | | | | | | | | |
| | | | 185 | | | | 190 | | | | | | 195 | | | 200 | | | | | | | | | | | | | |
| gtt | gtc | cca | gcc | gag | aag | ccg | ccg | ccg | tcg | tcc | ggc | tca | aat | ttc | gtg | 736 | | | | | | | | | | | | | |
| Val | Val | Pro | Ala | Glu | Lys | Pro | Pro | Pro | Ser | Ser | Gly | Ser | Asn | Phe | Val | | | | | | | | | | | | | | |
| | | | 205 | | | | | | | 210 | | | | | | 215 | | | | | | | | | | | | | |
| gtc | tcg | gct | tct | gct | ccc | agg | ctg | gac | att | gac | agc | gat | gtt | gaa | cct | 784 | | | | | | | | | | | | | |
| Val | Ser | Ala | Ser | Ala | Pro | Arg | Leu | Asp | Ile | Asp | Ser | Asp | Val | Glu | Pro | | | | | | | | | | | | | | |
| | | | 220 | | | | | | | 225 | | | | | | 230 | | | | | | | | | | | | | |
| gaa | ctg | aag | aag | ggt | gcg | gtc | atc | gtc | gaa | gaa | gct | cca | aac | cca | aag | 832 | | | | | | | | | | | | | |
| Glu | Leu | Lys | Lys | Gly | Ala | Val | Ile | Val | Glu | Glu | Ala | Pro | Asn | Pro | Lys | | | | | | | | | | | | | | |
| | | | 235 | | | | 240 | | | | | | 245 | | | | | | | | | | | | | | | | |
| gct | ctt | tcg | ccg | cct | gca | gcc | ccc | gct | gta | caa | gaa | gac | ctt | tgg | gac | 880 | | | | | | | | | | | | | |
| Ala | Leu | Ser | Pro | Pro | Ala | Ala | Pro | Ala | Val | Gln | Glu | Asp | Leu | Trp | Asp | | | | | | | | | | | | | | |
| | | | 250 | | | | 255 | | | | | | 260 | | | | | | | | | | | | | | | | |
| ttc | aag | aaa | tac | att | ggc | ttc | gag | gag | ccc | gtg | gag | gcc | aag | gat | gat | 928 | | | | | | | | | | | | | |
| Phe | Lys | Lys | Tyr | Ile | Gly | Phe | Glu | Glu | Pro | Val | Glu | Ala | Lys | Asp | Asp | | | | | | | | | | | | | | |
| | | | 265 | | | | 270 | | | | | | 275 | | | 280 | | | | | | | | | | | | | |
| ggc | tgg | gct | gtt | gca | gat | gat | gcg | ggc | tcc | ttt | gaa | cat | cac | cag | aac | 976 | | | | | | | | | | | | | |
| Gly | Trp | Ala | Val | Ala | Asp | Asp | Ala | Gly | Ser | Phe | Glu | His | His | Gln | Asn | | | | | | | | | | | | | | |
| | | | 285 | | | | | | | 290 | | | | | | 295 | | | | | | | | | | | | | |
| cat | gat | tcc | gga | cct | ttg | gca | ggg | gag | aac | gtc | atg | aac | gtg | gtc | gtc | 1024 | | | | | | | | | | | | | |
| His | Asp | Ser | Gly | Pro | Leu | Ala | Gly | Glu | Asn | Val | Met | Asn | Val | Val | Val | | | | | | | | | | | | | | |
| | | | 300 | | | | | | | 305 | | | | | | 310 | | | | | | | | | | | | | |
| gtg | gct | gct | gaa | tgt | tct | ccc | tgg | tgc | aaa | aca | ggg | ggg | ctt | gga | gat | 1072 | | | | | | | | | | | | | |
| Val | Ala | Ala | Glu | Cys | Ser | Pro | Trp | Cys | Lys | Thr | Gly | Gly | Leu | Gly | Asp | | | | | | | | | | | | | | |
| | | | 315 | | | | 320 | | | | | | 325 | | | | | | | | | | | | | | | | |
| gtt | gcc | ggt | gct | ttg | ccc | aag | gct | ttg | gcg | aag | aga | gga | cat | cgt | gtt | 1120 | | | | | | | | | | | | | |
| Val | Ala | Gly | Ala | Leu | Pro | Lys | Ala | Leu | Ala | Lys | Arg | Gly | His | Arg | Val | | | | | | | | | | | | | | |
| | | | 330 | | | | 335 | | | | | | 340 | | | | | | | | | | | | | | | | |
| atg | gtt | gtg | gta | cca | agg | tat | ggg | gac | | | | | | | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| cct Pro | ctc Leu | ttc Phe 395 | cga Arg | cac His | cgc Arg | cag Gln | gaa Glu 400 | gac Asp | att Ile | tat Tyr | ggg Gly | ggc Gly 405 | agc Ser | aga Arg | cag Gln | 1312 |
| gaa Glu | att Ile 410 | atg Met | aag Lys | cgc Arg | atg Met | att Ile 415 | ttg Leu | ttc Phe | tgc Cys | aag Lys | gcc Ala 420 | gct Ala | gtc Val | gag Glu | gtt Val | 1360 |
| cct Pro 425 | tgg Trp | cac His | gtt Val | cca Pro | tgc Cys 430 | ggc Gly | ggg Gly | gtc Val | cct Pro | tat Tyr 435 | ggg Gly | gat Asp | gga Gly | aat Asn | ctg Leu 440 | 1408 |
| gtg Val | ttt Phe | att Ile | gca Ala 445 | aat Asn | gat Asp | tgg Trp | cac His | acg Thr | gca Ala 450 | ctc Leu | ctg Leu | cct Pro | gtc Val | tat Tyr 455 | ctg Leu | 1456 |
| aaa Lys | gca Ala | tat Tyr 460 | tac Tyr | agg Arg | gac Asp | cat His | ggg Gly | ttg Leu 465 | atg Met | cag Gln | tac Tyr | act Thr | cgg Arg 470 | tcc Ser | att Ile | 1504 |
| atg Met | gtg Val | ata Ile 475 | cat His | aac Asn | atc Ile | gcg Ala | cac His 480 | cag Gln | ggc Gly | cgt Arg | ggc Gly | cca Pro 485 | gta Val | gat Asp | gaa Glu | 1552 |
| ttc Phe 490 | ccg Pro | ttc Phe | acc Thr | gag Glu | ttg Leu | cct Pro 495 | gag Glu | cac His | tac Tyr | ctg Leu | gaa Glu 500 | cac His | ttc Phe | aga Arg | ctg Leu | 1600 |
| tac Tyr 505 | gac Asp | ccc Pro | gtg Val | ggg Gly | ggg Gly 510 | gag Glu | cac His | gcc Ala | aac Asn | tac Tyr 515 | ttc Phe | gcc Ala | gcc Ala | ggc Gly | ctg Leu 520 | 1648 |
| aag Lys | atg Met | gcg Ala | gac Asp | cag Gln 525 | gtt Val | gtc Val | gtg Val | gtg Val | agc Ser 530 | ccc Pro | ggg Gly | tac Tyr | ctg Leu | tgg Trp 535 | gag Glu | 1696 |
| ctc Leu | aag Lys | acg Thr | gtg Val 540 | gag Glu | ggc Gly | ggc Gly | tgg Trp | ggg Gly 545 | ctt Leu | cac His | gac Asp | atc Ile | ata Ile 550 | cgg Arg | cag Gln | 1744 |
| aac Asn | gac Asp | tgg Trp 555 | aag Lys | acc Thr | cgc Arg | ggc Gly | atc Ile 560 | gtc Val | aac Asn | ggc Gly | atc Ile | gac Asp 565 | aac Asn | atg Met | gag Glu | 1792 |
| tgg Trp 570 | aac Asn | ccc Pro | gag Glu | gtg Val | gac Asp | gtc Val 575 | cac His | ctc Leu | aag Lys | tgc Ser | gac Asp 580 | ggc Gly | tac Tyr | acc Thr | aac Asn | 1840 |
| ttc Phe 585 | tcc Ser | ctg Leu | ggg Gly | acg Thr | ctg Leu 590 | gac Asp | tcc Ser | ggc Gly | aag Lys | cgg Arg 595 | cag Gln | tgc Cys | aag Lys | gag Glu | gcc Ala 600 | 1888 |
| ctg Leu | cag Gln | cgc Arg | gag Glu 605 | ctg Leu | ggc Gly | ctg Leu | cag Gln | gtc Val | cgc Arg 610 | gcc Ala | gac Asp | gtg Val | ccg Pro | ctg Leu 615 | ctc Leu | 1936 |
| ggc Gly | ttc Phe | atc Ile 620 | ggc Gly | cgc Arg | ctg Leu | gac Asp | ggg Gly | cag Gln 625 | aag Lys | ggc Gly | gtg Val | gag Glu | atc Ile 630 | atc Ile | gcg Ala | 1984 |
| gac Asp | gcc Ala | atg Met 635 | ccc Pro | tgg Trp | atc Ile | gtg Val | agc Ser 640 | cag Gln | gac Asp | gtg Val | cag Gln | ctg Leu 645 | gtc Val | atg Met | ctg Leu | 2032 |

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Pro His Ala Gly Ala Gly Arg Leu His Trp Pro Pro Trp Pro Pro Gln
35 40 45

Arg Thr Ala Arg Asp Gly Gly Val Ala Ala Arg Ala Ala Gly Lys Lys
50 55 60

Asp Ala Arg Val Asp Asp Asp Ala Ala Ser Ala Arg Gln Pro Arg Ala
65 70 75 80

Arg Arg Gly Gly Ala Ala Thr Lys Val Ala Glu Arg Arg Asp Pro Val
85 90 95

Lys Thr Leu Asp Arg Asp Ala Ala Glu Gly Gly Ala Pro Ala Pro Pro
100 105 110

Ala Pro Arg Gln Asp Ala Ala Arg Pro Pro Ser Met Asn Gly Thr Pro
115 120 125

Val Asn Gly Glu Asn Lys Ser Thr Gly Gly Gly Gly Ala Thr Lys Asp
130 135 140

Ser Gly Leu Pro Ala Pro Ala Arg Ala Pro His Pro Ser Thr Gln Asn
145 150 155 160

Arg Val Pro Val Asn Gly Glu Asn Lys Ala Asn Val Ala Ser Pro Pro
165 170 175

Thr Ser Ile Ala Glu Val Val Ala Pro Asp Ser Ala Ala Thr Ile Ser
180 185 190

Ile Ser Asp Lys Ala Pro Glu Ser Val Val Pro Ala Glu Lys Pro Pro
195 200 205

Pro Ser Ser Gly Ser Asn Phe Val Val Ser Ala Ser Ala Pro Arg Leu
210 215 220

Asp Ile Asp Ser Asp Val Glu Pro Glu Leu Lys Lys Gly Ala Val Ile
225 230 235 240

Val Glu Glu Ala Pro Asn Pro Lys Ala Leu Ser Pro Pro Ala Ala Pro
245 250 255

Ala Val Gln Glu Asp Leu Trp Asp Phe Lys Lys Tyr Ile Gly Phe Glu
260 265 270

Glu Pro Val Glu Ala Lys Asp Asp Gly Trp Ala Val Ala Asp Asp Ala
275 280 285

Gly Ser Phe Glu His His Gln Asn His Asp Ser Gly Pro Leu Ala Gly
290 295 300

Glu Asn Val Met Asn Val Val Val Val Ala Ala Glu Cys Ser Pro Trp
305 310 315 320

Cys Lys Thr Gly Gly Leu Gly Asp Val Ala Gly Ala Leu Pro Lys Ala
325 330 335

Leu Ala Lys Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr Gly
340 345 350

Asp Tyr Glu Glu Ala Tyr Asp Val Gly Val Arg Lys Tyr Tyr Lys Ala
355 360 365

Ala Gly Gln Asp Met Glu Val Asn Tyr Phe His Ala Tyr Ile Asp Gly
370 375 380

| | | | | | | | | | | | | | | | | |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val 385 | Asp | Phe | Val | Phe | Ile | Asp | Ala | Pro | Leu | Phe | Arg | His | Arg | Gln | Glu | 400 |
| Asp | Ile | Tyr | Gly | Gly | Ser | Arg | Gln | Glu | Ile | Met | Lys | Arg | Met | Ile | Leu | 415 |
| Phe | Cys | Lys | Ala | Ala | Val | Glu | Val | Pro | Trp | His | Val | Pro | Cys | Gly | Gly | 425 |
| Val | Pro | Tyr | Gly | Asp | Gly | Asn | Leu | Val | Phe | Ile | Ala | Asn | Asp | Trp | His | 435 |
| Thr | Ala | Leu | Leu | Pro | Val | Tyr | Leu | Lys | Ala | Tyr | Tyr | Arg | Asp | His | Gly | 445 |
| Leu | Met | Gln | Tyr | Thr | Arg | Ser | Ile | Met | Val | Ile | His | Asn | Ile | Ala | His | 455 |
| Gln | Gly | Arg | Gly | Pro | Val | Asp | Glu | Phe | Pro | Phe | Thr | Glu | Leu | Pro | Glu | 465 |
| His | Tyr | Leu | Glu | His | Phe | Arg | Leu | Tyr | Asp | Pro | Val | Gly | Gly | Glu | His | 475 |
| Ala | Asn | Tyr | Phe | Ala | Ala | Gly | Leu | Lys | Met | Ala | Asp | Gln | Val | Val | Val | 485 |
| Val | Ser | Pro | Gly | Tyr | Leu | Trp | Glu | Leu | Lys | Thr | Val | Glu | Gly | Gly | Trp | 495 |
| Gly | Leu | His | Asp | Ile | Ile | Arg | Gln | Asn | Asp | Trp | Lys | Thr | Arg | Gly | Ile | 505 |
| Val | Asn | Gly | Ile | Asp | Asn | Met | Glu | Trp | Asn | Pro | Glu | Val | Asp | Val | His | 515 |
| Leu | Lys | Ser | Asp | Gly | Tyr | Thr | Asn | Phe | Ser | Leu | Gly | Thr | Leu | Asp | Ser | 525 |
| Gly | Lys | Arg | Gln | Cys | Lys | Glu | Ala | Leu | Gln | Arg | Glu | Leu | Gly | Leu | Gln | 535 |
| Val | Arg | Ala | Asp | Val | Pro | Leu | Leu | Gly | Phe | Ile | Gly | Arg | Leu | Asp | Gly | 545 |
| Gln | Lys | Gly | Val | Glu | Ile | Ile | Ala | Asp | Ala | Met | Pro | Trp | Ile | Val | Ser | 555 |
| Gln | Asp | Val | Gln | Leu | Val | Met | Leu | Gly | Thr | Gly | Arg | His | Asp | Leu | Glu | 565 |
| Ser | Met | Leu | Arg | His | Phe | Glu | Arg | Glu | His | His | Asp | Lys | Val | Arg | Gly | 575 |
| Trp | Val | Gly | Phe | Ser | Val | Arg | Leu | Ala | His | Arg | Ile | Thr | Ala | Gly | Ala | 585 |
| Asp | Ala | Leu | Leu | Met | Pro | Ser | Arg | Phe | Glu | Pro | Cys | Gly | Leu | Asn | Gln | 595 |
| Leu | Tyr | Ala | Met | Ala | Tyr | Gly | Thr | Val | Pro | Val | Val | His | Ala | Val | Gly | 605 |
| Gly | Val | Arg | Asp | Thr | Val | Pro | Pro | Phe | Asp | Pro | Phe | Asn | His | Ser | Gly | 615 |

| | | | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| <400> | 5 | | | | | | | | | | | | | | | | |
| cca | gct | gag | aag | acg | ccg | ccg | tcg | tcc | ggc | tca | aat | ttc | gag | tcc | tcg | | 48 |
| Pro | Ala | Glu | Lys | Thr | Pro | Pro | Ser | Ser | Gly | Ser | Asn | Phe | Glu | Ser | Ser | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |
| gcc | tct | gct | ccc | ggg | tct | gac | act | gtc | agc | gac | gtg | gaa | caa | gaa | ctg | | 96 |
| Ala | Ser | Ala | Pro | Gly | Ser | Asp | Thr | Val | Ser | Asp | Val | Glu | Gln | Glu | Leu | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| aag | aag | ggt | gcg | gtc | gtt | gtc | gaa | gaa | gct | cca | aag | cca | aag | gct | ctt | | 144 |
| Lys | Lys | Gly | Ala | Val | Val | Val | Glu | Glu | Ala | Pro | Lys | Pro | Lys | Ala | Leu | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| tcg | ccg | cct | gca | gcc | ccc | gct | gta | caa | gaa | gac | ctt | tgg | gat | ttc | aag | | 192 |
| Ser | Pro | Pro | Ala | Ala | Pro | Ala | Val | Gln | Glu | Asp | Leu | Trp | Asp | Phe | Lys | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| aaa | tac | att | ggt | ttc | gag | gag | ccc | gtg | gag | gcc | aag | gat | gat | ggc | cgg | | 240 |
| Lys | Tyr | Ile | Gly | Phe | Glu | Glu | Pro | Val | Glu | Ala | Lys | Asp | Asp | Gly | Arg | | |
| 65 | | | | 70 | | | | | 75 | | | | | | 80 | | |
| gct | gtc | gca | gat | gat | gcg | ggc | tcc | ttt | gaa | cac | cac | cag | aat | cac | gac | | 288 |
| Ala | Val | Ala | Asp | Asp | Ala | Gly | Ser | Phe | Glu | His | His | Gln | Asn | His | Asp | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | |
| tcc | gga | cct | ttg | gca | ggg | gag | aat | gtc | atg | aac | gtg | gtc | gtc | gtg | gct | | 336 |
| Ser | Gly | Pro | Leu | Ala | Gly | Glu | Asn | Val | Met | Asn | Val | Val | Val | Val | Ala | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| gct | gag | tgt | tct | ccc | tgg | tgc | aaa | aca | ggt | ggt | ctg | gga | gat | gtt | gcg | | 384 |
| Ala | Glu | Cys | Ser | Pro | Trp | Cys | Lys | Thr | Gly | Gly | Leu | Gly | Asp | Val | Ala | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| ggg | gct | ctg | ccc | aag | gct | ttg | gca | aag | aga | gga | cat | cgt | gtt | atg | gtt | | 432 |
| Gly | Ala | Leu | Pro | Lys | Ala | Leu | Ala | Lys | Arg | Gly | His | Arg | Val | Met | Val | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | |
| gtg | gta | cca | agg | tat | ggg | gac | tat | gaa | gaa | cct | acg | gat | gtc | gga | gtc | | 480 |
| Val | Val | Pro | Arg | Tyr | Gly | Asp | Tyr | Glu | Glu | Pro | Thr | Asp | Val | Gly | Val | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |

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PCT/AU00/00385

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| | |
|---|------|
| cga aaa tac tac aag gct gct gga cag gat atg gaa gtg aat tat ttc | 528 |
| Arg Lys Tyr Tyr Lys Ala Ala Gly Gln Asp Met Glu Val Asn Tyr Phe | |
| 165 170 175 | |
| cat gct tat atc gat gga gtt gat ttt gtg ttc att gac gct cct ctc | 576 |
| His Ala Tyr Ile Asp Gly Val Asp Phe Val Phe Ile Asp Ala Pro Leu | |
| 180 185 190 | |
| ttc cga cac cga gag gaa gac att tat ggg ggc agc aga cag gaa att | 624 |
| Phe Arg His Arg Glu Glu Asp Ile Tyr Gly Gly Ser Arg Gln Glu Ile | |
| 195 200 205 | |
| atg aag cgc atg att ttg ttc tgc aag gcc gct gtt gag gtt cca tgg | 672 |
| Met Lys Arg Met Ile Leu Phe Cys Lys Ala Ala Val Glu Val Pro Trp | |
| 210 215 220 | |
| cac gtt cca tgc ggc ggt gtc cct tat ggg gat gga aat ctg gtg ttt | 720 |
| His Val Pro Cys Gly Gly Val Pro Tyr Gly Asp Gly Asn Leu Val Phe | |
| 225 230 235 240 | |
| att gca aat gat tgg cac acg gca ctc ctg cct gtc tat ctg aaa gca | 768 |
| Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro Val Tyr Leu Lys Ala | |
| 245 250 255 | |
| tat tac agg gac cat ggt ttg atg cag tac act cgg tcc att atg gtg | 816 |
| Tyr Tyr Arg Asp His Gly Leu Met Gln Tyr Thr Arg Ser Ile Met Val | |
| 260 265 270 | |
| ata cat aac atc gct cac cag ggc cgt ggc cct gta gat gaa ttc ccg | 864 |
| Ile His Asn Ile Ala His Gln Gly Arg Gly Pro Val Asp Glu Phe Pro | |
| 275 280 285 | |
| ttc acc gag ttg cct gag cac tac ctg gaa cac ttc aga ctg tac gac | 912 |
| Phe Thr Glu Leu Pro Glu His Tyr Leu Glu His Phe Arg Leu Tyr Asp | |
| 290 295 300 | |
| ccc gtg ggt ggt gaa cac gcc aac tac ttc gcc gcc ggc ctg aag atg | 960 |
| Pro Val Gly Gly Glu His Ala Asn Tyr Phe Ala Ala Gly Leu Lys Met | |
| 305 310 315 320 | |
| gcg gac cag gtt gtc gtg gtg agc ccc ggg tac ctg tgg gag ctg aag | 1008 |
| Ala Asp Gln Val Val Val Val Ser Pro Gly Tyr Leu Trp Glu Leu Lys | |
| 325 330 335 | |
| acg gtg gag ggc ggc tgg ggg ctt cac gac atc ata cgg cag aac gac | 1056 |
| Thr Val Glu Gly Gly Trp Gly Leu His Asp Ile Ile Arg Gln Asn Asp | |
| 340 345 350 | |
| tgg aag acc cgc ggc atc gtc aac ggc atc gac aac atg gag tgg aac | 1104 |
| Trp Lys Thr Arg Gly Ile Val Asn Gly Ile Asp Asn Met Glu Trp Asn | |
| 355 360 365 | |
| ccc gag gtg gac gcc cac ctc aag tcg gac ggc tac acc aac ttc tcc | 1152 |
| Pro Glu Val Asp Ala His Leu Lys Ser Asp Gly Tyr Thr Asn Phe Ser | |
| 370 375 380 | |
| ctg agg acg ctg gac tcc ggc aag cgg cag tgc aag gag gcc ctg cag | 1200 |
| Leu Arg Thr Leu Asp Ser Gly Lys Arg Gln Cys Lys Glu Ala Leu Gln | |
| 385 390 395 400 | |
| cgc gag ctg ggc ctg cag gtc cgc gcc gac gtg ccg ctg ctc ggc ttc | 1248 |
| Arg Glu Leu Gly Leu Gln Val Arg Ala Asp Val Pro Leu Leu Gly Phe | |
| 405 410 415 | |
| atc ggc cgc ctg gac ggg cag aag ggc gtg gag atc atc gcg gac gcc | 1296 |

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Ile Gly Arg Leu Asp Gly Gln Lys Gly Val Glu Ile Ile Ala Asp Ala
420 425 430

atg ccc tgg atc gtg agc cag gac gtg cag ctg gtg atg ctg ggc acc 1344
Met Pro Trp Ile Val Ser Gln Asp Val Gln Leu Val Met Leu Gly Thr
435 440 445

ggg cgc cac gac ctg gag agc atg ctg cag cac ttc gag cgg gag cac 1392
Gly Arg His Asp Leu Glu Ser Met Leu Gln His Phe Glu Arg Glu His
450 455 460

cac gac aag gtg cgc ggg tgg gtg ggg ttc tcc gtg cgc ctg gcg cac 1440
His Asp Lys Val Arg Gly Trp Val Gly Phe Ser Val Arg Leu Ala His
465 470 475 480

cgg atc acg gcg ggg gcg gac gcg ctc ctc atg ccc tcc cgg ttc gtg 1488
Arg Ile Thr Ala Gly Ala Asp Ala Leu Leu Met Pro Ser Arg Phe Val
485 490 495

ccg tgc ggg ctg aac cag ctc tac gcc atg gcc tac ggc acc gtc ccc 1536
Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Ala Tyr Gly Thr Val Pro
500 505 510

gtc gtg cac gcc gtc ggc ggc ctc agg gac acc gtg ccg ccg ttc gac 1584
Val Val His Ala Val Gly Gly Leu Arg Asp Thr Val Pro Pro Phe Asp
515 520 525

ccc ttc aac cac tcc ggg ctc ggg tgg acg ttc gac cgc gcc gag gcg 1632
Pro Phe Asn His Ser Gly Leu Gly Trp Thr Phe Asp Arg Ala Glu Ala
530 535 540

cac aag ctg atc gag gcg ctc ggg cac tgc ctc cgc acc tac cga gac 1680
His Lys Leu Ile Glu Ala Leu Gly His Cys Leu Arg Thr Tyr Arg Asp
545 550 555 560

ttc aag gag agc tgg agg gcc ctc cag gag cgc ggc atg tgc cag gac 1728
Phe Lys Glu Ser Trp Arg Ala Leu Gln Arg Gly Met Ser Gln Asp
565 570 575

ttc agc tgg gag cac gcc gcc aag ctc tac gag gac gtc ctc gtc aag 1776
Phe Ser Trp Glu His Ala Ala Lys Leu Tyr Glu Asp Val Leu Val Lys
580 585 590

gcc aag tac cag tgg tgaacgctag ctgctagccg ctccagcccc gcatgcgtgc 1831
Ala Lys Tyr Gln Trp
595

atgacaggat ggaactgcat tgcgcacgca ggaaagtgcc atggagcgcc ggcattccgcg 1891

aagtacagtg acatgaggtg tgtgtggttg agacgtgat tccaatccgg cccgtagcag 1951

agtagagcgg aggtatatgg gaattttaac ttgttattgt aatttggttat gttgtgtgca 2011

ttattacaat gttgttactt attcttggtta agtcggaggc caagggcgaa agctagctca 2071

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| | | | |
|---|-----|-----|-----|
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| Ala Ser Ala Pro Gly Ser Asp Thr Val Ser Asp Val Glu Gln Glu Leu | 20 | 25 | 30 |
| Lys Lys Gly Ala Val Val Val Glu Glu Ala Pro Lys Pro Lys Ala Leu | 35 | 40 | 45 |
| Ser Pro Pro Ala Ala Pro Ala Val Gln Glu Asp Leu Trp Asp Phe Lys | 50 | 55 | 60 |
| Lys Tyr Ile Gly Phe Glu Glu Pro Val Glu Ala Lys Asp Asp Gly Arg | 65 | 70 | 75 |
| Ala Val Ala Asp Asp Ala Gly Ser Phe Glu His His Gln Asn His Asp | 85 | 90 | 95 |
| Ser Gly Pro Leu Ala Gly Glu Asn Val Met Asn Val Val Val Val Ala | 100 | 105 | 110 |
| Ala Glu Cys Ser Pro Trp Cys Lys Thr Gly Gly Leu Gly Asp Val Ala | 115 | 120 | 125 |
| Gly Ala Leu Pro Lys Ala Leu Ala Lys Arg Gly His Arg Val Met Val | 130 | 135 | 140 |
| Val Val Pro Arg Tyr Gly Asp Tyr Glu Glu Pro Thr Asp Val Gly Val | 145 | 150 | 155 |
| Arg Lys Tyr Tyr Lys Ala Ala Gly Gln Asp Met Glu Val Asn Tyr Phe | 165 | 170 | 175 |
| His Ala Tyr Ile Asp Gly Val Asp Phe Val Phe Ile Asp Ala Pro Leu | 180 | 185 | 190 |
| Phe Arg His Arg Glu Glu Asp Ile Tyr Gly Gly Ser Arg Gln Glu Ile | 195 | 200 | 205 |
| Met Lys Arg Met Ile Leu Phe Cys Lys Ala Ala Val Glu Val Pro Trp | 210 | 215 | 220 |
| His Val Pro Cys Gly Gly Val Pro Tyr Gly Asp Gly Asn Leu Val Phe | 225 | 230 | 235 |
| Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro Val Tyr Leu Lys Ala | 245 | 250 | 255 |
| Tyr Tyr Arg Asp His Gly Leu Met Gln Tyr Thr Arg Ser Ile Met Val | 260 | 265 | 270 |
| Ile His Asn Ile Ala His Gln Gly Arg Gly Pro Val Asp Glu Phe Pro | 275 | 280 | 285 |
| Phe Thr Glu Leu Pro Glu His Tyr Leu Glu His Phe Arg Leu Tyr Asp | 290 | 295 | 300 |
| Pro Val Gly Gly Glu His Ala Asn Tyr Phe Ala Ala Gly Leu Lys Met | 305 | 310 | 315 |
| Ala Asp Gln Val Val Val Val Ser Pro Gly Tyr Leu Trp Glu Leu Lys | 325 | 330 | 335 |
| Thr Val Glu Gly Gly Trp Gly Leu His Asp Ile Ile Arg Gln Asn Asp | 340 | 345 | 350 |

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Trp Lys Thr Arg Gly Ile Val Asn Gly Ile Asp Asn Met Glu Trp Asn
 355 360 365
 Pro Glu Val Asp Ala His Leu Lys Ser Asp Gly Tyr Thr Asn Phe Ser
 370 375 380
 Leu Arg Thr Leu Asp Ser Gly Lys Arg Gln Cys Lys Glu Ala Leu Gln
 385 390 395 400
 Arg Glu Leu Gly Leu Gln Val Arg Ala Asp Val Pro Leu Leu Gly Phe
 405 410 415
 Ile Gly Arg Leu Asp Gly Gln Lys Gly Val Glu Ile Ile Ala Asp Ala
 420 425 430
 Met Pro Trp Ile Val Ser Gln Asp Val Gln Leu Val Met Leu Gly Thr
 435 440 445
 Gly Arg His Asp Leu Glu Ser Met Leu Gln His Phe Glu Arg Glu His
 450 455 460
 His Asp Lys Val Arg Gly Trp Val Gly Phe Ser Val Arg Leu Ala His
 465 470 475 480
 Arg Ile Thr Ala Gly Ala Asp Ala Leu Leu Met Pro Ser Arg Phe Val
 485 490 495
 Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Ala Tyr Gly Thr Val Pro
 500 505 510
 Val Val His Ala Val Gly Gly Leu Arg Asp Thr Val Pro Pro Phe Asp
 515 520 525
 Pro Phe Asn His Ser Gly Leu Gly Trp Thr Phe Asp Arg Ala Glu Ala
 530 535 540
 His Lys Leu Ile Glu Ala Leu Gly His Cys Leu Arg Thr Tyr Arg Asp
 545 550 555 560
 Phe Lys Glu Ser Trp Arg Ala Leu Gln Glu Arg Gly Met Ser Gln Asp
 565 570 575
 Phe Ser Trp Glu His Ala Ala Lys Leu Tyr Glu Asp Val Leu Val Lys
 580 585 590
 Ala Lys Tyr Gln Trp
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 1 5

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 Ser Pro Leu Cys Pro Arg Ser Arg Gln Pro Leu Val Val Val Arg Pro

| | | | | | | | | | | | | | | | | | | | | | | | |
|---|-----|--|--|--|--|--|--|--|--|--|----|--|--|--|--|--|--|--|--|--|--|----|--|
| 10 | | | | | | | | | | | 15 | | | | | | | | | | | 20 | |
| gcc ggc cgc ggc ggc ctc acg cag cct ttt ttg atg aat ggc aga ttt | 148 | | | | | | | | | | | | | | | | | | | | | | |
| Ala Gly Arg Gly Gly Leu Thr Gln Pro Phe Leu Met Asn Gly Arg Phe | | | | | | | | | | | | | | | | | | | | | | | |
| 25 30 35 40 | | | | | | | | | | | | | | | | | | | | | | | |
| act cga agc agg acc ctt cga tgc atg gta gca agt tca gat cct cct | 196 | | | | | | | | | | | | | | | | | | | | | | |
| Thr Arg Ser Arg Thr Leu Arg Cys Met Val Ala Ser Ser Asp Pro Pro | | | | | | | | | | | | | | | | | | | | | | | |
| 45 50 55 | | | | | | | | | | | | | | | | | | | | | | | |
| aat agg aaa tca aga agg atg gta cca cct cag gtt aaa gtc att tct | 244 | | | | | | | | | | | | | | | | | | | | | | |
| Asn Arg Lys Ser Arg Arg Met Val Pro Pro Gln Val Lys Val Ile Ser | | | | | | | | | | | | | | | | | | | | | | | |
| 60 65 70 | | | | | | | | | | | | | | | | | | | | | | | |
| tct aga gga tat acg aca aga ctc att gtt gaa cca agc aac gag aat | 292 | | | | | | | | | | | | | | | | | | | | | | |
| Ser Arg Gly Tyr Thr Thr Arg Leu Ile Val Glu Pro Ser Asn Glu Asn | | | | | | | | | | | | | | | | | | | | | | | |
| 75 80 85 | | | | | | | | | | | | | | | | | | | | | | | |
| aca gaa cac aat aat cgg gat gaa gaa act ctt gat aca tac aat gcg | 340 | | | | | | | | | | | | | | | | | | | | | | |
| Thr Glu His Asn Asn Arg Asp Glu Glu Thr Leu Asp Thr Tyr Asn Ala | | | | | | | | | | | | | | | | | | | | | | | |
| 90 95 100 | | | | | | | | | | | | | | | | | | | | | | | |
| cta tta agt acc gag aca gca gaa tgg aca gat aat aga gaa gcc gag | 388 | | | | | | | | | | | | | | | | | | | | | | |
| Leu Leu Ser Thr Glu Thr Ala Glu Trp Thr Asp Asn Arg Glu Ala Glu | | | | | | | | | | | | | | | | | | | | | | | |
| 105 110 115 120 | | | | | | | | | | | | | | | | | | | | | | | |
| act gct aaa gcg gac tcg tcg caa aat gct tta agc agt tct ata att | 436 | | | | | | | | | | | | | | | | | | | | | | |
| Thr Ala Lys Ala Asp Ser Ser Gln Asn Ala Leu Ser Ser Ser Ile Ile | | | | | | | | | | | | | | | | | | | | | | | |
| 125 130 135 | | | | | | | | | | | | | | | | | | | | | | | |
| ggg gaa gtg gat gtg gcg gat gaa gat ata ctt gcg gct gat ctg aca | 484 | | | | | | | | | | | | | | | | | | | | | | |
| Gly Glu Val Asp Val Ala Asp Glu Asp Ile Leu Ala Ala Asp Leu Thr | | | | | | | | | | | | | | | | | | | | | | | |
| 140 145 150 | | | | | | | | | | | | | | | | | | | | | | | |
| gtg tat tca ttg agc agt gta atg aag aag gaa gtg gat gca gcg gac | 532 | | | | | | | | | | | | | | | | | | | | | | |
| Val Tyr Ser Leu Ser Ser Val Met Lys Lys Glu Val Asp Ala Ala Asp | | | | | | | | | | | | | | | | | | | | | | | |
| 155 160 165 | | | | | | | | | | | | | | | | | | | | | | | |
| aaa gct aga gtt aaa gaa gac gca ttt gag ctg gat ttg cca gca act | 580 | | | | | | | | | | | | | | | | | | | | | | |
| Lys Ala Arg Val Lys Glu Asp Ala Phe Glu Leu Asp Leu Pro Ala Thr | | | | | | | | | | | | | | | | | | | | | | | |
| 170 175 180 | | | | | | | | | | | | | | | | | | | | | | | |
| aca ttg aga agt gtg ata gta gat gtg atg gat cat aat ggg act gta | 628 | | | | | | | | | | | | | | | | | | | | | | |
| Thr Leu Arg Ser Val Ile Val Asp Val Met Asp His Asn Gly Thr Val | | | | | | | | | | | | | | | | | | | | | | | |
| 185 190 195 200 | | | | | | | | | | | | | | | | | | | | | | | |
| caa gag aca ttg aga agt gtg ata gta gat gtg atg gat cat aat ggg | 676 | | | | | | | | | | | | | | | | | | | | | | |
| Gln Glu Thr Leu Arg Ser Val Ile Val Asp Val Met Asp His Asn Gly | | | | | | | | | | | | | | | | | | | | | | | |
| 205 210 215 | | | | | | | | | | | | | | | | | | | | | | | |
| act gta caa gag aca ttg aga agt gtg ata gta gat gtg atg gat gat | 724 | | | | | | | | | | | | | | | | | | | | | | |
| Thr Val Gln Glu Thr Leu Arg Ser Val Ile Val Asp Val Met Asp Asp | | | | | | | | | | | | | | | | | | | | | | | |
| 220 225 230 | | | | | | | | | | | | | | | | | | | | | | | |
| gcg gcg gac aaa gct aga gtt gaa gaa gac gta ttt gag ctg gat ttg | 772 | | | | | | | | | | | | | | | | | | | | | | |
| Ala Ala Asp Lys Ala Arg Val Glu Glu Asp Val Phe Glu Leu Asp Leu | | | | | | | | | | | | | | | | | | | | | | | |
| 235 240 245 | | | | | | | | | | | | | | | | | | | | | | | |
| tca gga aat att tca agc agt gcg acg acc gtg gaa cta gat gcg gtt | 820 | | | | | | | | | | | | | | | | | | | | | | |
| Ser Gly Asn Ile Ser Ser Ser Ala Thr Thr Val Glu Leu Asp Ala Val | | | | | | | | | | | | | | | | | | | | | | | |
| 250 255 260 | | | | | | | | | | | | | | | | | | | | | | | |
| gac gaa gtc ggg cct gtt caa gac aaa ttt gag gcg acc tca tca gga | 868 | | | | | | | | | | | | | | | | | | | | | | |
| Asp Glu Val Gly Pro Val Gln Asp Lys Phe Glu Ala Thr Ser Ser Gly | | | | | | | | | | | | | | | | | | | | | | | |
| 265 270 275 280 | | | | | | | | | | | | | | | | | | | | | | | |

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| | |
|---|------|
| aat gtt tca aac agt gca acg gta cgg gaa gtg gat gca agt gat gaa | 916 |
| Asn Val Ser Asn Ser Ala Thr Val Arg Glu Val Asp Ala Ser Asp Glu | |
| 285 290 295 | |
| gct ggg aat gat caa ggc ata ttt aga gca gat ttg tca gga aat gtt | 964 |
| Ala Gly Asn Asp Gln Gly Ile Phe Arg Ala Asp Leu Ser Gly Asn Val | |
| 300 305 310 | |
| ttt tca agc agt aca aca gtg gaa gtg ggt gca gtg gat gaa gct ggg | 1012 |
| Phe Ser Ser Ser Thr Thr Val Glu Val Gly Ala Val Asp Glu Ala Gly | |
| 315 320 325 | |
| tct ata aag gac agg ttt gag acg gat tcg tca gga aat gtt tca aca | 1060 |
| Ser Ile Lys Asp Arg Phe Glu Thr Asp Ser Ser Gly Asn Val Ser Thr | |
| 330 335 340 | |
| agt gcg ccg atg tgg gat gca att gat gaa acc gtg gct gat caa gac | 1108 |
| Ser Ala Pro Met Trp Asp Ala Ile Asp Glu Thr Val Ala Asp Gln Asp | |
| 345 350 355 360 | |
| aca ttt gag gcg gat ttg tcg gga aat gct tca agc tgc gca aca tac | 1156 |
| Thr Phe Glu Ala Asp Leu Ser Gly Asn Ala Ser Ser Cys Ala Thr Tyr | |
| 365 370 375 | |
| aga gaa gtg gat gat gtg gtg gat gaa act aga tca gaa gag gaa aca | 1204 |
| Arg Glu Val Asp Val Val Asp Glu Thr Arg Ser Glu Glu Glu Thr | |
| 380 385 390 | |
| ttt gca atg gat ttg ttt gca agt gaa tca ggc cat gag aaa cat atg | 1252 |
| Phe Ala Met Asp Leu Phe Ala Ser Glu Ser Gly His Glu Lys His Met | |
| 395 400 405 | |
| gca gtg gat tat gtg ggt gaa gct acc gat gaa gaa gag act tac caa | 1300 |
| Ala Val Asp Tyr Val Gly Glu Ala Thr Asp Glu Glu Glu Thr Tyr Gln | |
| 410 415 420 | |
| cag caa tat cca gta ccg tct tca ttc tct atg tgg gac aag gct att | 1348 |
| Gln Gln Tyr Pro Val Pro Ser Ser Phe Ser Met Trp Asp Lys Ala Ile | |
| 425 430 435 440 | |
| gct aaa aca ggt gta agt ttg aat cct gag ctg cga ctt gtc agg gtt | 1396 |
| Ala Lys Thr Gly Val Ser Leu Asn Pro Glu Leu Arg Leu Val Arg Val | |
| 445 450 455 | |
| gaa gaa caa ggc aaa gta aat ttt agt gat aaa aaa gac ctg tca att | 1444 |
| Glu Glu Gln Gly Lys Val Asn Phe Ser Asp Lys Lys Asp Leu Ser Ile | |
| 460 465 470 | |
| gat gat tta cca gga caa aac caa tcg atc att ggt tcc tat aaa caa | 1492 |
| Asp Asp Leu Pro Gly Gln Asn Gln Ser Ile Ile Gly Ser Tyr Lys Gln | |
| 475 480 485 | |
| gat aaa tca att gct gat gtt gcg gga ccg acc caa tca att ttt ggt | 1540 |
| Asp Lys Ser Ile Ala Asp Val Ala Gly Pro Thr Gln Ser Ile Phe Gly | |
| 490 495 500 | |
| tct agt aaa caa cac ccg tca att gtt gct ttc ccc aaa caa aac cag | 1588 |
| Ser Ser Lys Gln His Arg Ser Ile Val Ala Phe Pro Lys Gln Asn Gln | |
| 505 510 515 520 | |
| tca att gtt agt gtc act gag caa aag cag tcc ata gtt gga ttc cgt | 1636 |
| Ser Ile Val Ser Val Thr Glu Gln Lys Gln Ser Ile Val Gly Phe Arg | |
| 525 530 535 | |

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agt caa gat ctt tcg gct gtt agt ctc cct aaa caa aac gta cca att 1684
 Ser Gln Asp Leu Ser Ala Val Ser Leu Pro Lys Gln Asn Val Pro Ile
 540 545 550

gtt ggt acg tcg aga gag ggt caa aca aag caa gtt cct gtt gtt gat 1732
 Val Gly Thr Ser Arg Glu Gly Gln Thr Lys Gln Val Pro Val Val Asp
 555 560 565

aga cag gat gca ttg tat gtg aat gga ctg gaa gct aag gag gga gat 1780
 Arg Gln Asp Ala Leu Tyr Val Asn Gly Leu Glu Ala Lys Glu Gly Asp
 570 575 580

cac aca tcc gag aaa act gat gag gat gcg ctt cat gta aag ttt aat 1828
 His Thr Ser Glu Lys Thr Asp Glu Asp Ala Leu His Val Lys Phe Asn
 585 590 595 600

gtt gac aat gtg ttg cgg aag cat cag gca gat aga acc caa gca gtg 1876
 Val Asp Asn Val Leu Arg Lys His Gln Ala Asp Arg Thr Gln Ala Val
 605 610 615

gaa aag aaa act tgg aag aaa gtt gat gag gaa cat ctt tac atg act 1924
 Glu Lys Lys Thr Trp Lys Lys Val Asp Glu Glu His Leu Tyr Met Thr
 620 625 630

gaa cat cag aaa cgt gct gcc gaa gga cag atg gta gtt aac gag gat 1972
 Glu His Gln Lys Arg Ala Ala Glu Gly Gln Met Val Val Asn Glu Asp
 635 640 645

gag ctt tct ata act gaa att gga atg ggg aga ggt gat aaa att cag 2020
 Glu Leu Ser Ile Thr Glu Ile Gly Met Gly Arg Gly Asp Lys Ile Gln
 650 655 660

cat gtg ctt tct gag gaa gag ctt tca tgg tct gaa gat gaa gtg cag 2068
 His Val Leu Ser Glu Glu Glu Leu Ser Trp Ser Glu Asp Glu Val Gln
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tta att gag gat gat gga caa tat gaa gtt gac gag acc tct gtg tcc 2116
 Leu Ile Glu Asp Asp Gly Gln Tyr Glu Val Asp Glu Thr Ser Val Ser
 685 690 695

gtt aac gtt gaa caa gat atc cag ggg tca cca cag gat gtt gtg gat 2164
 Val Asn Val Glu Gln Asp Ile Gln Gly Ser Pro Gln Asp Val Val Asp
 700 705 710

ccg caa gca cta aag gtg atg ctg caa gaa ctc gct gag aaa aat tat 2212
 Pro Gln Ala Leu Lys Val Met Leu Gln Glu Leu Ala Glu Lys Asn Tyr
 715 720 725

tcg atg agg aac aag ctg ttt gtt ttt cca gag gta gtg aaa gct gat 2260
 Ser Met Arg Asn Lys Leu Phe Val Phe Pro Glu Val Val Lys Ala Asp
 730 735 740

tca gtt att gat ctt tat tta aat cgt gac cta aca gct ttg gcg aat 2308
 Ser Val Ile Asp Leu Tyr Leu Asn Arg Asp Leu Thr Ala Leu Ala Asn
 745 750 755 760

gaa ccc gat gtc gtc atc aaa gga gca ttc aat ggt tgg aaa tgg agg 2356
 Glu Pro Asp Val Val Ile Lys Gly Ala Phe Asn Gly Trp Lys Trp Arg
 765 770 775

ctt ttc act gaa aga ttg cac aag agt gac ctt gga ggg gtt tgg tgg 2404
 Leu Phe Thr Glu Arg Leu His Lys Ser Asp Leu Gly Gly Val Trp Trp
 780 785 790

tct tgc aaa ctg tac ata ccc aag gag gcc tac aga tta gac ttt gtg 2452

| | | | | | | | | | | | | | | | | |
|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|------|------|
| Ser | Cys | Lys 795 | Leu | Tyr | Ile | Pro | Lys 800 | Glu | Ala | Tyr | Arg | Leu 805 | Asp | Phe | Val | |
| ttc | ttc | aac | ggt | cgc | acg | gtc | tat | gag | aac | aat | ggc | aac | aat | gat | ttc | 2500 |
| Phe | Phe | Asn | Gly | Arg | Thr | Val | Tyr | Glu | Asn | Asn | Gly | Asn | Asn | Asp | Phe | |
| | 810 | | | | | 815 | | | | | 820 | | | | | |
| tgt | ata | gga | ata | gaa | ggc | act | atg | aat | gaa | gat | ctg | ttt | gag | gat | ttc | 2548 |
| Cys | Ile | Gly | Ile | Glu | Gly | Thr | Met | Asn | Glu | Asp | Leu | Phe | Glu | Asp | Phe | |
| 825 | | | | | 830 | | | | | 835 | | | | | 840 | |
| ttg | gtt | aaa | gaa | aag | caa | agg | gag | ctt | gag | aaa | ctt | gcc | atg | gaa | gaa | 2596 |
| Leu | Val | Lys | Glu | Lys | Gln | Arg | Glu | Leu | Glu | Lys | Leu | Ala | Met | Glu | Glu | |
| | | | | 845 | | | | | 850 | | | | | 855 | | |
| gct | gaa | agg | agg | aca | cag | act | gaa | gaa | cag | cgg | cga | aga | aag | gaa | gca | 2644 |
| Ala | Glu | Arg | Arg | Thr | Gln | Thr | Glu | Glu | Gln | Arg | Arg | Arg | Lys | Glu | Ala | |
| | | | 860 | | | | | 865 | | | | | 870 | | | |
| agg | gct | gca | gat | gaa | gct | gtc | agg | gca | caa | gcg | aag | gcc | gag | ata | gag | 2692 |
| Arg | Ala | Ala | Asp | Glu | Ala | Val | Arg | Ala | Gln | Ala | Lys | Ala | Glu | Ile | Glu | |
| | | 875 | | | | | 880 | | | | | 885 | | | | |
| atc | aag | aag | aaa | aaa | ttg | caa | agt | atg | ttg | agt | ttg | gcc | aga | aca | tgt | 2740 |
| Ile | Lys | Lys | Lys | Lys | Leu | Gln | Ser | Met | Leu | Ser | Leu | Ala | Arg | Thr | Cys | |
| | 890 | | | | | 895 | | | | | 900 | | | | | |
| gtt | gat | aat | ttg | tgg | tac | ata | gag | gct | agc | aca | gat | aca | aga | gga | gat | 2788 |
| Val | Asp | Asn | Leu | Trp | Tyr | Ile | Glu | Ala | Ser | Thr | Asp | Thr | Arg | Gly | Asp | |
| 905 | | | | | 910 | | | | 915 | | | | | | 920 | |
| act | atc | agg | tta | tat | tat | aac | aga | aac | tcg | agg | cca | ctt | gcg | cat | agt | 2836 |
| Thr | Ile | Arg | Leu | Tyr | Tyr | Asn | Arg | Asn | Ser | Arg | Pro | Leu | Ala | His | Ser | |
| | | | | 925 | | | | | 930 | | | | | 935 | | |
| act | gag | att | tgg | atg | cat | ggt | ggt | tac | aac | aat | tgg | aca | gat | gga | ctc | 2884 |
| Thr | Glu | Ile | Trp | Met | His | Gly | Gly | Tyr | Asn | Asn | Trp | Thr | Asp | Gly | Leu | |
| | | | 940 | | | | 945 | | | | | | 950 | | | |
| tct | att | gtt | gaa | agc | ttt | gtc | aag | tgc | aat | gac | aaa | gac | ggc | gat | tgg | 2932 |
| Ser | Ile | Val | Glu | Ser | Phe | Val | Lys | Cys | Asn | Asp | Lys | Asp | Gly | Asp | Trp | |
| | | 955 | | | | | 960 | | | | | 965 | | | | |
| tgg | tat | gca | gat | gtt | att | cca | cct | gaa | aag | gca | ctt | gtg | ttg | gac | tgg | 2980 |
| Trp | Tyr | Ala | Asp | Val | Ile | Pro | Pro | Glu | Lys | Ala | Leu | Val | Leu | Asp | Trp | |
| | 970 | | | | | 975 | | | | | 980 | | | | | |
| gtt | ttt | gct | gat | ggg | cca | gct | ggg | aat | gca | agg | aac | tat | gac | aac | aat | 3028 |
| Val | Phe | Ala | Asp | Gly | Pro | Ala | Gly | Asn | Ala | Arg | Asn | Tyr | Asp | Asn | Asn | |
| 985 | | | | | 990 | | | | | 995 | | | | | 1000 | |
| gct | cga | caa | gat | ttc | cat | gct | att | ctt | ccg | aac | aac | aat | gta | acc | gag | 3076 |
| Ala | Arg | Gln | Asp | Phe | His | Ala | Ile | Leu | Pro | Asn | Asn | Asn | Val | Thr | Glu | |
| | | | | | | | | | | | | | | | | |

| | | | |
|---|------|------|------|
| 1050 | 1055 | 1060 | |
| ctg ctt tcc cag aaa cac att gtt tat acc gaa ccg ctt gaa ata cgt | | | 3268 |
| Leu Leu Ser Gln Lys His Ile Val Tyr Thr Glu Pro Leu Glu Ile Arg | | | |
| 1065 | 1070 | 1075 | 1080 |
| gcc gga acc aca gtg gat gtg cta tac aat ccc tct aac aca gtg cta | | | 3316 |
| Ala Gly Thr Thr Val Asp Val Leu Tyr Asn Pro Ser Asn Thr Val Leu | | | |
| | 1085 | 1090 | 1095 |
| aat gga aag tcc gag ggt tgg ttt aga tgc tcc ttt aac ctt tgg atg | | | 3364 |
| Asn Gly Lys Ser Glu Gly Trp Phe Arg Cys Ser Phe Asn Leu Trp Met | | | |
| | 1100 | 1105 | 1110 |
| cat tca agt ggg gca ttg cca ccc cag aag atg gtg aaa tca ggg gat | | | 3412 |
| His Ser Ser Gly Ala Leu Pro Pro Gln Lys Met Val Lys Ser Gly Asp | | | |
| | 1115 | 1120 | 1125 |
| ggg ccg ctc tta aaa gca aca gtt gat gtt cca ccg gat gcc tat atg | | | 3460 |
| Gly Pro Leu Leu Lys Ala Thr Val Asp Val Pro Pro Asp Ala Tyr Met | | | |
| | 1130 | 1135 | 1140 |
| atg gac ttt gtt ttc tcc gag tgg gaa gaa gat ggg atc tat gac aac | | | 3508 |
| Met Asp Phe Val Phe Ser Glu Trp Glu Glu Asp Gly Ile Tyr Asp Asn | | | |
| 1145 | 1150 | 1155 | 1160 |
| agg aat ggg atg gac tat cat att cct gtt tct gat tca att gaa aca | | | 3556 |
| Arg Asn Gly Met Asp Tyr His Ile Pro Val Ser Asp Ser Ile Glu Thr | | | |
| | 1165 | 1170 | 1175 |
| gag aat tac atg cgt att atc cac att gcc gtt gag atg gcc ccc gtt | | | 3604 |
| Glu Asn Tyr Met Arg Ile Ile His Ile Ala Val Glu Met Ala Pro Val | | | |
| | 1180 | 1185 | 1190 |
| gca aag gtt gga ggt ctt ggg gat gtt gtt aca agt ctt tca cgt gcc | | | 3652 |
| Ala Lys Val Gly Gly Leu Gly Asp Val Val Thr Ser Leu Ser Arg Ala | | | |
| | 1195 | 1200 | 1205 |
| att caa gat cta gga cat act gtc gag gtt att ctc ccg aag tac gac | | | 3700 |
| Ile Gln Asp Leu Gly His Thr Val Glu Val Ile Leu Pro Lys Tyr Asp | | | |
| | 1210 | 1215 | 1220 |
| tgt ttg aac caa agc agt gtc aag gat tta cat tta tat caa agt ttt | | | 3748 |
| Cys Leu Asn Gln Ser Ser Val Lys Asp Leu His Leu Tyr Gln Ser Phe | | | |
| 1225 | 1230 | 1235 | 1240 |
| tct tgg ggt ggt aca gaa ata aaa gta tgg gtt gga cga gtc gaa gac | | | 3796 |
| Ser Trp Gly Gly Thr Glu Ile Lys Val Trp Val Gly Arg Val Glu Asp | | | |
| | 1245 | 1250 | 1255 |
| ctg acc gtt tac ttc ctg gaa cct caa aat ggg atg ttt ggc gtt gga | | | 3844 |
| Leu Thr Val Tyr Phe Leu Glu Pro Gln Asn Gly Met Phe Gly Val Gly | | | |
| | 1260 | 1265 | 1270 |
| tgt gta tat gga agg aat gat gac cgc aga ttt ggg ttc ttc tgt cat | | | 3892 |
| Cys Val Tyr Gly Arg Asn Asp Asp Arg Arg Phe Gly Phe Phe Cys His | | | |
| | 1275 | 1280 | 1285 |
| tct gct cta gag ttt atc ctc cag aat gaa ttt tct cca cat ata ata | | | 3940 |
| Ser Ala Leu Glu Phe Ile Leu Gln Asn Glu Phe Ser Pro His Ile Ile | | | |
| | 1290 | 1295 | 1300 |
| cat tgc cat gat tgg tca agt gct ccg gtc gcc tgg cta tat aag gaa | | | 3988 |
| His Cys His Asp Trp Ser Ser Ala Pro Val Ala Trp Leu Tyr Lys Glu | | | |
| 1305 | 1310 | 1315 | 1320 |

| | |
|---|------|
| cac tat tcc caa tcc aga atg gca agc act cgg gtt gta ttt acc atc | 4036 |
| His Tyr Ser Gln Ser Arg Met Ala Ser Thr Arg Val Val Phe Thr Ile | |
| 1325 1330 1335 | |
| cac aat ctt gaa ttt gga gca cat tat att ggt aaa gca atg aca tac | 4084 |
| His Asn Leu Glu Phe Gly Ala His Tyr Ile Gly Lys Ala Met Thr Tyr | |
| 1340 1345 1350 | |
| tgt gat aaa gcc aca act gtt tct cct aca tat tca agg gac gtg gca | 4132 |
| Cys Asp Lys Ala Thr Thr Val Ser Pro Thr Tyr Ser Arg Asp Val Ala | |
| 1355 1360 1365 | |
| ggc cat ggc gcc att gct cct cat cgt gag aaa ttc tac ggc att ctc | 4180 |
| Gly His Gly Ala Ile Ala Pro His Arg Glu Lys Phe Tyr Gly Ile Leu | |
| 1370 1375 1380 | |
| aat gga att gat cca gat atc tgg gat ccg tac act gac aat ttt atc | 4228 |
| Asn Gly Ile Asp Pro Asp Ile Trp Asp Pro Tyr Thr Asp Asn Phe Ile | |
| 1385 1390 1400 | |
| ccg gtc cct tat act tgt gag aat gtt gtc gaa ggc aag aga gct gca | 4276 |
| Pro Val Pro Tyr Thr Cys Glu Asn Val Val Glu Gly Lys Arg Ala Ala | |
| 1405 1410 1415 | |
| aaa agg gcc ttg cag cag aag ttt gga tta cag caa act gat gtc cct | 4324 |
| Lys Arg Ala Leu Gln Gln Lys Phe Gly Leu Gln Gln Thr Asp Val Pro | |
| 1420 1425 1430 | |
| att gtc gga atc atc acc cgt ctg aca gcc cag aag gga atc cac ctc | 4372 |
| Ile Val Gly Ile Ile Thr Arg Leu Thr Ala Gln Lys Gly Ile His Leu | |
| 1435 1440 1445 | |
| atc aag cac gca att cac cga act ctc gaa agc aac gga cat gtg gtt | 4420 |
| Ile Lys His Ala Ile His Arg Thr Leu Glu Ser Asn Gly His Val Val | |
| 1450 1455 1460 | |
| ttg ctt ggt tca gct cca gat cat cga ata caa ggc gat ttt tgc aga | 4468 |
| Leu Leu Gly Ser Ala Pro Asp His Arg Ile Gln Gly Asp Phe Cys Arg | |
| 1465 1470 1475 1480 | |
| ttg gcc gat gct ctt cat ggt gtt tac cat ggt agg gtg aag ctt gtt | 4516 |
| Leu Ala Asp Ala Leu His Gly Val Tyr His Gly Arg Val Lys Leu Val | |
| 1485 1490 1495 | |
| cta acc tat gat gag cct ctt tct cac ctg ata tac gct ggc tcg gac | 4564 |
| Leu Thr Tyr Asp Glu Pro Leu Ser His Leu Ile Tyr Ala Gly Ser Asp | |
| 1500 1505 1510 | |
| ttc ata att gtt cct tca atc ttc gaa ccc tgt ggc tta aca caa ctt | 4612 |
| Phe Ile Ile Val Pro Ser Ile Phe Glu Pro Cys Gly Leu Thr Gln Leu | |
| 1515 1520 1525 | |
| gtt gcc atg cgt tat gga tcg atc cct ata gtt cgg aaa act gga gga | 4660 |
| Val Ala Met Arg Tyr Gly Ser Ile Pro Ile Val Arg Lys Thr Gly Gly | |
| 1530 1535 1540 | |
| ctt cac gac aca gtc ttc gac gta gac aat gat aag gac cgg gct cgg | 4708 |
| Leu His Asp Thr Val Phe Asp Val Asp Asn Asp Lys Asp Arg Ala Arg | |
| 1545 1550 1555 1560 | |
| tct ctt ggt ctt gaa cca aat ggg ttc agt ttc gac gga gcc gac agc | 4756 |
| Ser Leu Gly Leu Glu Pro Asn Gly Phe Ser Phe Asp Gly Ala Asp Ser | |
| 1565 1570 1575 | |

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aat ggc gtg gat tat gcc ctc aac aga gca atc ggc gct tgg ttc gat 4804
Asn Gly Val Asp Tyr Ala Leu Asn Arg Ala Ile Gly Ala Trp Phe Asp
      1580                      1585                      1590

gcc cgt gat tgg ttc cac tcc ctg tgt aag agg gtc atg gag caa gac 4852
Ala Arg Asp Trp Phe His Ser Leu Cys Lys Arg Val Met Glu Gln Asp
      1595                      1600                      1605

tgg tcg tgg aac cgg ccc gca ctg gac tac att gaa ttg tac cat gcc 4900
Trp Ser Trp Asn Arg Pro Ala Leu Asp Tyr Ile Glu Leu Tyr His Ala
      1610                      1615                      1620

gct cga aaa ttc tgacacccaa ctgaaccaat gacaagaaca agcgcatgtg 4952
Ala Arg Lys Phe
1625

gggatcgact agtcatacag ggctgtgcag atcgtcttgc ttcagttagt gccctcttca 5012

gttagttcca agcgcaactac agtcgtacat agctgaggat cctcttgcct cctaccaggg 5072

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gatatttaca tttgtggaaa aaaaaaaaaa aaaa 5346

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<213> Triticum aestivum

<400> 8
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Gln Pro Leu Val Val Val Arg Pro Ala Gly Arg Gly Gly Leu Thr Gln
      20              25              30

Pro Phe Leu Met Asn Gly Arg Phe Thr Arg Ser Arg Thr Leu Arg Cys
      35              40              45

Met Val Ala Ser Ser Asp Pro Pro Asn Arg Lys Ser Arg Arg Met Val
      50              55              60

Pro Pro Gln Val Lys Val Ile Ser Ser Arg Gly Tyr Thr Thr Arg Leu
      65              70              75              80

Ile Val Glu Pro Ser Asn Glu Asn Thr Glu His Asn Asn Arg Asp Glu
      85              90              95

Glu Thr Leu Asp Thr Tyr Asn Ala Leu Leu Ser Thr Glu Thr Ala Glu
      100             105             110

Trp Thr Asp Asn Arg Glu Ala Glu Thr Ala Lys Ala Asp Ser Ser Gln
      115             120             125

Asn Ala Leu Ser Ser Ser Ile Ile Gly Glu Val Asp Val Ala Asp Glu
      130             135             140

Asp Ile Leu Ala Ala Asp Leu Thr Val Tyr Ser Leu Ser Ser Val Met

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|---------------------|-----------------|-----------------|-----------------|---------|---------|-----|
| 145 | | 150 | | 155 | | 160 |
| Lys Lys Glu Val Asp | Ala Ala Asp | Lys Ala Arg Val | Lys Glu Asp | Ala | | |
| | 165 | | 170 | | 175 | |
| Phe Glu Leu Asp | Leu Pro Ala Thr | Thr Leu Arg Ser | Val Ile Val Asp | | | |
| | 180 | | 185 | | 190 | |
| Val Met Asp His Asn | Gly Thr Val | Gln Glu Thr Leu | Arg Ser Val | Ile | | |
| | 195 | | 200 | | 205 | |
| Val Asp Val Met Asp | His Asn Gly Thr | Val Gln Glu Thr | Leu Arg Ser | | | |
| | 210 | | 215 | | 220 | |
| Val Ile Val Asp Val | Met Asp Asp | Ala Ala Asp | Lys Ala Arg | Val Glu | | |
| | 225 | | 230 | | 235 | |
| Glu Asp Val Phe | Glu Leu Asp | Leu Ser Gly | Asn Ile Ser | Ser Ser | Ala | |
| | 245 | | 250 | | 255 | |
| Thr Thr Val Glu | Leu Asp Ala | Val Asp Glu | Val Gly Pro | Val Gln | Asp | |
| | 260 | | 265 | | 270 | |
| Lys Phe Glu Ala Thr | Ser Ser Gly | Asn Val Ser | Asn Ser | Ala Thr | Val | |
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| Arg Glu Val Asp | Ala Ser Asp | Glu Ala Gly | Asn Asp | Gln Gly | Ile Phe | |
| | 290 | | 295 | | 300 | |
| Arg Ala Asp Leu | Ser Gly Asn | Val Phe Ser | Ser Ser | Thr Thr | Val Glu | |
| | 305 | | 310 | | 315 | |
| Val Gly Ala Val | Asp Glu Ala | Gly Ser Ile | Lys Asp | Arg Phe | Glu Thr | |
| | 325 | | 330 | | 335 | |
| Asp Ser Ser Gly | Asn Val Ser | Thr Ser | Ala Pro | Met Trp | Asp Ala | Ile |
| | 340 | | 345 | | 350 | |
| Asp Glu Thr Val | Ala Asp Gln | Asp Thr | Phe Glu | Ala Asp | Leu Ser | Gly |
| | 355 | | 360 | | 365 | |
| Asn Ala Ser Ser | Cys Ala Thr | Tyr Arg | Glu Val | Asp Asp | Val Val | Asp |
| | 370 | | 375 | | 380 | |
| Glu Thr Arg Ser | Glu Glu Glu | Thr Phe | Ala Met | Asp Leu | Phe Ala | Ser |
| | 385 | | 390 | | 395 | |
| Glu Ser Gly His | Glu Lys His | Met Ala | Val Asp | Tyr Val | Gly Glu | Ala |
| | 405 | | 410 | | 415 | |
| Thr Asp Glu Glu | Glu Thr Tyr | Gln Gln | Gln Tyr | Pro Val | Pro Ser | Ser |
| | 420 | | 425 | | 430 | |
| Phe Ser Met Trp | Asp Lys Ala | Ile Ala | Lys Thr | Gly Val | Ser Leu | Asn |
| | 435 | | 440 | | 445 | |
| Pro Glu Leu Arg | Leu Val Arg | Val Glu | Glu Gln | Gly Lys | Val Asn | Phe |
| | 450 | | 455 | | 460 | |
| Ser Asp Lys Lys | Asp Leu Ser | Ile Asp | Asp Leu | Pro Gly | Gln Asn | Gln |
| | 465 | | 470 | | 475 | |
| Ser Ile Ile Gly | Ser Tyr Lys | Gln Asp | Lys Ser | Ile Ala | Asp Val | Ala |
| | 485 | | 490 | | 495 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Thr | Gln | Ser | Ile | Phe | Gly | Ser | Lys | Gln | His | Arg | Ser | Ile | |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Val | Ala | Phe | Pro | Lys | Gln | Asn | Gln | Ser | Ile | Val | Ser | Val | Thr | Glu | Gln |
| | | 515 | | | | | 520 | | | | | 525 | | | |
| Lys | Gln | Ser | Ile | Val | Gly | Phe | Arg | Ser | Gln | Asp | Leu | Ser | Ala | Val | Ser |
| | 530 | | | | | 535 | | | | | 540 | | | | |
| Leu | Pro | Lys | Gln | Asn | Val | Pro | Ile | Val | Gly | Thr | Ser | Arg | Glu | Gly | Gln |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| Thr | Lys | Gln | Val | Pro | Val | Val | Asp | Arg | Gln | Asp | Ala | Leu | Tyr | Val | Asn |
| | | | | 565 | | | | | 570 | | | | | 575 | |
| Gly | Leu | Glu | Ala | Lys | Glu | Gly | Asp | His | Thr | Ser | Glu | Lys | Thr | Asp | Glu |
| | | | 580 | | | | | 585 | | | | | 590 | | |
| Asp | Ala | Leu | His | Val | Lys | Phe | Asn | Val | Asp | Asn | Val | Leu | Arg | Lys | His |
| | | 595 | | | | | 600 | | | | | 605 | | | |
| Gln | Ala | Asp | Arg | Thr | Gln | Ala | Val | Glu | Lys | Lys | Thr | Trp | Lys | Lys | Val |
| | 610 | | | | | 615 | | | | | 620 | | | | |
| Asp | Glu | Glu | His | Leu | Tyr | Met | Thr | Glu | His | Gln | Lys | Arg | Ala | Ala | Glu |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 |
| Gly | Gln | Met | Val | Val | Asn | Glu | Asp | Glu | Leu | Ser | Ile | Thr | Glu | Ile | Gly |
| | | | | 645 | | | | | 650 | | | | | 655 | |
| Met | Gly | Arg | Gly | Asp | Lys | Ile | Gln | His | Val | Leu | Ser | Glu | Glu | Glu | Leu |
| | | | 660 | | | | | 665 | | | | 670 | | | |
| Ser | Trp | Ser | Glu | Asp | Glu | Val | Gln | Leu | Ile | Glu | Asp | Asp | Gly | Gln | Tyr |
| | | 675 | | | | | 680 | | | | | 685 | | | |
| Glu | Val | Asp | Glu | Thr | Ser | Val | Ser | Val | Asn | Val | Glu | Gln | Asp | Ile | Gln |
| | 690 | | | | | 695 | | | | | 700 | | | | |
| Gly | Ser | Pro | Gln | Asp | Val | Val | Asp | Pro | Gln | Ala | Leu | Lys | Val | Met | Leu |
| 705 | | | | | 710 | | | | | 715 | | | | | 720 |
| Gln | Glu | Leu | Ala | Glu | Lys | Asn | Tyr | Ser | Met | Arg | Asn | Lys | Leu | Phe | Val |
| | | | | 725 | | | | | 730 | | | | | 735 | |
| Phe | Pro | Glu | Val | Val | Lys | Ala | Asp | Ser | Val | Ile | Asp | Leu | Tyr | Leu | Asn |
| | | | 740 | | | | | 745 | | | | 750 | | | |
| Arg | Asp | Leu | Thr | Ala | Leu | Ala | Asn | Glu | Pro | Asp | Val | Val | Ile | Lys | Gly |
| | 755 | | | | | | 760 | | | | | 765 | | | |
| Ala | Phe | Asn | Gly | Trp | Lys | Trp | Arg | Leu | Phe | Thr | Glu | Arg | Leu | His | Lys |
| | 770 | | | | | 775 | | | | | 780 | | | | |
| Ser | Asp | Leu | Gly | Gly | Val | Trp | Trp | Ser | Cys | Lys | Leu | Tyr | Ile | Pro | Lys |
| 785 | | | | | 790 | | | | | 795 | | | | | 800 |
| Glu | Ala | Tyr | Arg | Leu | Asp | Phe | Val | Phe | Phe | Asn | Gly | Arg | Thr | Val | Tyr |
| | | | | 805 | | | | | 810 | | | | | 815 | |
| Glu | Asn | Asn | Gly | Asn | Asn | Asp | Phe | Cys | Ile | Gly | Ile | Glu | Gly | Thr | Met |
| | | | 820 | | | | | 825 | | | | | 830 | | |
| Asn | Glu | Asp | Leu | Phe | Glu | Asp | Phe | Leu | Val | Lys | Glu | Lys | Gln | Arg | Glu |
| | | 835 | | | | | 840 | | | | | 845 | | | |

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Leu Glu Lys Leu Ala Met Glu Glu Ala Glu Arg Arg Thr Gln Thr Glu
 850 855 860
 Glu Gln Arg Arg Arg Lys Glu Ala Arg Ala Ala Asp Glu Ala Val Arg
 865 870 875 880
 Ala Gln Ala Lys Ala Glu Ile Glu Ile Lys Lys Lys Lys Leu Gln Ser
 885 890 895
 Met Leu Ser Leu Ala Arg Thr Cys Val Asp Asn Leu Trp Tyr Ile Glu
 900 905 910
 Ala Ser Thr Asp Thr Arg Gly Asp Thr Ile Arg Leu Tyr Tyr Asn Arg
 915 920 925
 Asn Ser Arg Pro Leu Ala His Ser Thr Glu Ile Trp Met His Gly Gly
 930 935 940
 Tyr Asn Asn Trp Thr Asp Gly Leu Ser Ile Val Glu Ser Phe Val Lys
 945 950 955 960
 Cys Asn Asp Lys Asp Gly Asp Trp Trp Tyr Ala Asp Val Ile Pro Pro
 965 970 975
 Glu Lys Ala Leu Val Leu Asp Trp Val Phe Ala Asp Gly Pro Ala Gly
 980 985 990
 Asn Ala Arg Asn Tyr Asp Asn Asn Ala Arg Gln Asp Phe His Ala Ile
 995 1000 1005
 Leu Pro Asn Asn Asn Val Thr Glu Glu Gly Phe Trp Ala Gln Glu Glu
 1010 1015 1020
 Gln Asn Ile Tyr Thr Arg Leu Leu Gln Glu Arg Arg Glu Lys Glu Glu
 025 1030 1035 1040
 Thr Met Lys Arg Lys Ala Glu Arg Ser Ala Asn Ile Lys Ala Glu Met
 1045 1050 1055
 Lys Ala Lys Thr Met Arg Arg Phe Leu Leu Ser Gln Lys His Ile Val
 1060 1065 1070
 Tyr Thr Glu Pro Leu Glu Ile Arg Ala Gly Thr Thr Val Asp Val Leu
 1075 1080 1085
 Tyr Asn Pro Ser Asn Thr Val Leu Asn Gly Lys Ser Glu Gly Trp Phe
 1090 1095 1100
 Arg Cys Ser Phe Asn Leu Trp Met His Ser Ser Gly Ala Leu Pro Pro
 105 1110 1115 1120
 Gln Lys Met Val Lys Ser Gly Asp Gly Pro Leu Leu Lys Ala Thr Val
 1125 1130 1135
 Asp Val Pro Pro Asp Ala Tyr Met Met Asp Phe Val Phe Ser Glu Trp
 1140 1145 1150
 Glu Glu Asp Gly Ile Tyr Asp Asn Arg Asn Gly Met Asp Tyr His Ile
 1155 1160 1165
 Pro Val Ser Asp Ser Ile Glu Thr Glu Asn Tyr Met Arg Ile Ile His
 1170 1175 1180
 Ile Ala Val Glu Met Ala Pro Val Ala Lys Val Gly Gly Leu Gly Asp

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| | | | |
|---|------|------|------|
| 185 | 1190 | 1195 | 1200 |
| Val Val Thr Ser Leu Ser Arg Ala Ile Gln Asp Leu Gly His Thr Val | 1205 | 1210 | 1215 |
| Glu Val Ile Leu Pro Lys Tyr Asp Cys Leu Asn Gln Ser Ser Val Lys | 1220 | 1225 | 1230 |
| Asp Leu His Leu Tyr Gln Ser Phe Ser Trp Gly Gly Thr Glu Ile Lys | 1235 | 1240 | 1245 |
| Val Trp Val Gly Arg Val Glu Asp Leu Thr Val Tyr Phe Leu Glu Pro | 1250 | 1255 | 1260 |
| Gln Asn Gly Met Phe Gly Val Gly Cys Val Tyr Gly Arg Asn Asp Asp | 1265 | 1270 | 1275 |
| Arg Arg Phe Gly Phe Phe Cys His Ser Ala Leu Glu Phe Ile Leu Gln | 1285 | 1290 | 1295 |
| Asn Glu Phe Ser Pro His Ile Ile His Cys His Asp Trp Ser Ser Ala | 1300 | 1305 | 1310 |
| Pro Val Ala Trp Leu Tyr Lys Glu His Tyr Ser Gln Ser Arg Met Ala | 1315 | 1320 | 1325 |
| Ser Thr Arg Val Val Phe Thr Ile His Asn Leu Glu Phe Gly Ala His | 1330 | 1335 | 1340 |
| Tyr Ile Gly Lys Ala Met Thr Tyr Cys Asp Lys Ala Thr Thr Val Ser | 1345 | 1350 | 1355 |
| Pro Thr Tyr Ser Arg Asp Val Ala Gly His Gly Ala Ile Ala Pro His | 1365 | 1370 | 1375 |
| Arg Glu Lys Phe Tyr Gly Ile Leu Asn Gly Ile Asp Pro Asp Ile Trp | 1380 | 1385 | 1390 |
| Asp Pro Tyr Thr Asp Asn Phe Ile Pro Val Pro Tyr Thr Cys Glu Asn | 1395 | 1400 | 1405 |
| Val Val Glu Gly Lys Arg Ala Ala Lys Arg Ala Leu Gln Gln Lys Phe | 1410 | 1415 | 1420 |
| Gly Leu Gln Gln Thr Asp Val Pro Ile Val Gly Ile Ile Thr Arg Leu | 1425 | 1430 | 1435 |
| Thr Ala Gln Lys Gly Ile His Leu Ile Lys His Ala Ile His Arg Thr | 1445 | 1450 | 1455 |
| Leu Glu Ser Asn Gly His Val Val Leu Leu Gly Ser Ala Pro Asp His | 1460 | 1465 | 1470 |
| Arg Ile Gln Gly Asp Phe Cys Arg Leu Ala Asp Ala Leu His Gly Val | 1475 | 1480 | 1485 |
| Tyr His Gly Arg Val Lys Leu Val Leu Thr Tyr Asp Glu Pro Leu Ser | 1490 | 1495 | 1500 |
| His Leu Ile Tyr Ala Gly Ser Asp Phe Ile Ile Val Pro Ser Ile Phe | 1505 | 1510 | 1515 |
| Glu Pro Cys Gly Leu Thr Gln Leu Val Ala Met Arg Tyr Gly Ser Ile | 1525 | 1530 | 1535 |

| | | | | | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|-----|
| <400> | 9 | | | | | | | | | | | | | | | | | | |
| gat | gca | tgt | tat | gtg | aat | gga | ctg | gaa | gct | aag | gag | gga | gat | cac | aca | | | | 48 |
| Asp | Ala | Leu | Tyr | Val | Asn | Gly | Leu | Glu | Ala | Lys | Glu | Gly | Asp | His | Thr | | | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | | | |
| tcc | gag | aaa | act | gat | gag | gat | gcg | ctt | cat | gta | aag | ttt | aat | gtt | gac | | | | 96 |
| Ser | Glu | Lys | Thr | Asp | Glu | Asp | Ala | Leu | His | Val | Lys | Phe | Asn | Val | Asp | | | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | | | |
| aat | gtg | tgt | cgg | aag | cat | cag | gca | gat | aga | acc | caa | gca | gtg | gaa | aag | | | | 144 |
| Asn | Val | Leu | Arg | Lys | His | Gln | Ala | Asp | Arg | Thr | Gln | Ala | Val | Glu | Lys | | | | |
| | | | 35 | | | | 40 | | | | | 45 | | | | | | | |
| aaa | act | tgg | aag | aaa | gtt | gat | gag | gaa | cat | ctt | tac | atg | act | gaa | cat | | | | 192 |
| Lys | Thr | Trp | Lys | Lys | Val | Asp | Glu | Glu | His | Leu | Try | Met | Thr | Glu | His | | | | |
| | | | 50 | | | 55 | | | | | 60 | | | | | | | | |
| cag | aaa | cgt | gct | gcc | gaa | gga | cag | atg | gta | gtt | aac | gag | gat | gag | ctt | | | | 240 |
| Gln | Lys | Arg | Ala | Ala | Glu | Gly | Gln | Met | Val | Val | Asn | Glu | Asp | Glu | Leu | | | | |
| -65 | . | | | | 70 | | | | | 75 | | | | | 80 | | | | |
| tct | ata | act | gaa | att | gga | atg | ggg | aga | ggt | gat | aaa | att | cag | cat | gtg | | | | 288 |
| Ser | Ile | Thr | Glu | Ile | Gly | Met | Gly | Arg | Gly | Asp | Lys | Ile | Gln | His | Val | | | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | | | |
| ctt | tct | gag | gaa | gag | ctt | tca | tgg | tct | gaa | gat | gaa | gtg | cag | tta | att | | | | 336 |
| Leu | Ser | Glu | Glu | Glu | Leu | Ser | Trp | Ser | Glu | Asp | Glu | Val | Gln | Leu | Ile | | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | | | |
| gag | gat | gat | gga | caa | tat | gaa | gtt | gac | gag | acc | tct | gtg | tcc | gtt | aac | | | | 384 |
| Glu | Asp | Asp | Gly | Gln | Tyr | Glu | Val | Asp | Glu | Thr | Ser | Val | Ser | Val | Asn | | | | |
| | | | 115 | | | | 120 | | | | | 125 | | | | | | | |
| gtt | gaa | caa | gat | atc | cag | ggg | tca | cca | cag | gat | gtt | gtg | gat | ccg | caa | | | | 432 |
| Val | Glu | Gln | Asp | Ile | Gln | Gly | Ser | Pro | Gln | Asp | Val | Val | Asp | Pro | Gln | | | | |
| | | | 130 | | | 135 | | | | | 140 | | | | | | | | |

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gca cta aag gtg atg ctg caa gaa ctc gct gag aaa aat tat tcg atg 480
 Ala Leu Lys Val Met Leu Gln Glu Leu Ala Glu Lys Asn Tyr Ser Met
 145 150 155 160

agg aac aag ctg ttt gtt ttt cca gag gta gtg aaa gct gat tca gtt 528
 Arg Asn Lys Leu Phe Val Phe Pro Glu Val Val Lys Ala Asp Ser Val
 165 170 175

att gat ctt tat tta aat cgt gac cta aca gct ttg gcg aat gaa ccc 576
 Ile Asp Leu Tyr Leu Asn Arg Asp Leu Thr Ala Leu Ala Asn Glu Pro
 180 185 190

gat gtc gtc atc aaa gga gca ttc aat ggt tgg aaa tgg agg ctt ttc 624
 Asp Val Val Ile Lys Gly Ala Phe Asn Gly Trp Lys Trp Arg Leu Phe
 195 200 205

act gaa aga ttg cac aag agt gac ctt gga ggg gtt tgg tgg tct tgc 672
 Thr Glu Arg Leu His Lys Ser Asp Leu Gly Gly Val Trp Trp Ser Cys
 210 215 220

aaa ctg tac ata ccc aag gag gcc tac aga tta gac ttt gtg ttc ttc 720
 Lys Leu Tyr Ile Pro Lys Glu Ala Tyr Arg Leu Asp Phe Val Phe Phe
 225 230 235 240

aac ggt cgc acg gtc tat gag aac aat ggc aac aat gat ttc tgt ata 768
 Asn Gly Arg Thr Val Tyr Glu Asn Asn Gly Asn Asn Asp Phe Cys Ile
 245 250 255

gga ata gaa ggc act atg aat gaa gat ctg ttt gag gat ttc ttg gtt 816
 Gly Ile Glu Gly Thr Met Asn Glu Asp Leu Phe Glu Asp Phe Leu Val
 260 265 270

aaa gaa aag caa agg gag ctt gag aaa ctt gcc atg gaa gaa gct gaa 864
 Lys Glu Lys Gln Arg Glu Leu Glu Lys Leu Ala Met Glu Glu Ala Glu
 275 280 285

agg agg aca cag act gaa gaa cag cgg cga aga aag gaa gca agg gct 912
 Arg Arg Thr Gln Thr Glu Glu Gln Arg Arg Arg Lys Glu Ala Arg Ala
 290 295 300

gca gat gaa gct gtc agg gca caa gcg aag gcc gag ata gag atc aag 960
 Ala Asp Glu Ala Val Arg Ala Gln Ala Lys Ala Glu Ile Glu Ile Lys
 305 310 315 320

aag aaa aaa ttg caa agt atg ttg agt ttg gcc aga aca tgt gtt gat 1008
 Lys Lys Lys Leu Gln Ser Met Leu Ser Leu Ala Arg Thr Cys Val Asp
 325 330 335

aat ttg tgg tac ata gag gct agc aca gat aca aga gga gat act atc 1056
 Asn Leu Trp Tyr Ile Glu Ala Ser Thr Asp Thr Arg Gly Asp Thr Ile
 340 345 350

agg tta tat tat aac aga aac tcg agg cca ctt gcg cat agt act gag 1104
 Arg Leu Tyr Tyr Asn Arg Asn Ser Arg Pro Leu Ala His Ser Thr Glu
 355 360 365

att tgg atg cat ggt ggt tac aac aat tgg tca gat gga ctc tct att 1152
 Ile Trp Met His Gly Gly Tyr Asn Asn Trp Ser Asp Gly Leu Ser Ile
 370 375 380

gtt gaa agc ttt gtc aag tgc aat gac aaa gac ggc gat tgg tgg tat 1200
 Val Glu Ser Phe Val Lys Cys Asn Asp Lys Asp Gly Asp Trp Trp Tyr
 385 390 395 400

gca gat gtt att cca cct gaa aag gca ctt gtg ttg gac tgg gtt ttt 1248

| Ala | Asp | Val | Ile | Pro | Glu | Lys | Ala | Leu | Val | Leu | Asp | Trp | Val | Phe | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| | | | | 405 | | | | | 410 | | | | | 415 | | | |
| gct | gat | ggg | cca | gct | ggg | aat | gca | agg | aac | tat | gac | aac | aat | gct | cga | 1296 | |
| Ala | Asp | Gly | Pro | Ala | Gly | Asn | Ala | Arg | Asn | Tyr | Asp | Asn | Asn | Ala | Arg | | |
| | | | | 420 | | | | | 425 | | | | | 430 | | | |
| caa | gat | ttc | cat | gct | att | ctt | ccg | aac | aac | aat | gta | acc | gag | gaa | ggc | 1344 | |
| Gln | Asp | Phe | His | Ala | Ile | Leu | Pro | Asn | Asn | Asn | Val | Thr | Glu | Glu | Gly | | |
| | | | | 435 | | | | | 440 | | | | | 445 | | | |
| ttc | tgg | gcg | caa | gag | gag | caa | aac | atc | tat | aca | agg | ctt | ctg | caa | gaa | 1392 | |
| Phe | Trp | Ala | Gln | Glu | Glu | Gln | Asn | Ile | Tyr | Thr | Arg | Leu | Leu | Gln | Glu | | |
| | | | | 450 | | | | | 455 | | | | | 460 | | | |
| agg | aga | gaa | aag | gaa | gaa | acc | atg | aaa | aga | aag | gct | gag | aga | agt | gca | 1440 | |
| Arg | Arg | Glu | Lys | Glu | Glu | Thr | Met | Lys | Arg | Lys | Ala | Glu | Arg | Ser | Ala | | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | | |
| aat | atc | aaa | gct | gag | atg | aag | gca | aaa | act | atg | cga | agg | ttt | ctg | ctt | 1488 | |
| Asn | Ile | Lys | Ala | Glu | Met | Lys | Ala | Lys | Thr | Met | Arg | Arg | Phe | Leu | Leu | | |
| | | | | 485 | | | | | 490 | | | | | 495 | | | |
| tcc | cag | aaa | cac | att | gtt | tat | acc | cga | acc | gnc | ttg | aaa | tac | gtg | ccc | 1536 | |
| Ser | Gln | Lys | His | Ile | Val | Tyr | Thr | Arg | Thr | Xaa | Leu | Lys | Tyr | Val | Pro | | |
| | | | | 500 | | | | | 505 | | | | | 510 | | | |
| gga | acc | aca | gtg | gat | gtg | cta | tac | aat | ccc | tct | aac | aca | gtg | cta | aat | 1584 | |
| Gly | Thr | Thr | Val | Asp | Val | Leu | Tyr | Asn | Pro | Ser | Asn | Thr | Val | Leu | Asn | | |
| | | | | 515 | | | | | 520 | | | | | 525 | | | |
| gga | aag | tcg | gag | ggt | tgg | ttt | aga | tgc | tcc | ttt | aac | ctt | tgg | atg | cat | 1632 | |
| Gly | Lys | Ser | Glu | Gly | Trp | Phe | Arg | Cys | Ser | Phe | Asn | Leu | Trp | Met | His | | |
| | | | | 530 | | | | | 535 | | | | | 540 | | | |
| tca | agt | ggg | gca | ttg | cca | ccc | cag | aag | atg | gtg | aaa | tca | ggg | gat | ggg | 1680 | |
| Ser | Ser | Gly | Ala | Leu | Pro | Pro | Gln | Lys | Met | Val | Lys | Ser | Gly | Asp | Gly | | |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 | | |
| ccg | ctc | tta | aaa | gca | aca | gtt | gat | gtt | cca | ccg | gat | gcc | tat | atg | atg | 1728 | |
| Pro | Leu | Leu | Lys | Ala | Thr | Val | Asp | Val | Pro | Pro | Asp | Ala | Tyr | Met | Met | | |
| | | | | 565 | | | | | 570 | | | | | 575 | | | |
| gac | ttt | gtt | ttc | tcc | gag | tgg | gaa | gaa | gat | ggg | atc | tat | gac | aac | agg | 1776 | |
| Asp | Phe | Val | Phe | Ser | Glu | Trp | Glu | Glu | Asp | Gly | Ile | Tyr | Asp | Asn | Arg | | |
| | | | | 580 | | | | | 585 | | | | | 590 | | | |
| aat | ggg | atg | gac | tat | cat | att | cct | gtt | tct | gat | tca | att | gaa | aca | gag | 1824 | |
| Asn | Gly | Met | Asp | Tyr | His | Ile | Pro | Val | Ser | Asp | Ser | Ile | Glu | Thr | Glu | | |
| | | | | 595 | | | | | 600 | | | | | 605 | | | |
| aat | tac | atg | cgt | att | atc | cac | att | gcc | gtt | gag | atg | gcc | ccc | gtt | gca | 1872 | |
| Asn | Tyr | Met | Arg | Ile | Ile | His | Ile | Ala | Val | Glu | Met | Ala | Pro | Val | Ala | | |
| | | | | 610 | | | | | 615 | | | | | 620 | | | |
| aag | gtt | gga | ggt | ctt | ggg | gat | gtt | gtt | aca | agt | ctt | tca | cgt | gcc | att | 1920 | |
| Lys | Val | Gly | Gly | Leu | Gly | | | | | | | | | | | | |

| 660 | | | | | | | | 665 | | | | 670 | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|--|--|--|
| tgg | ggt | ggt | aca | gaa | ata | aaa | gta | tgg | ggt | gga | cga | gtc | gaa | gac | ctg | 2064 | | | | |
| Trp | Gly | Gly | Thr | Glu | Ile | Lys | Val | Trp | Val | Gly | Arg | Val | Glu | Asp | Leu | | | | | |
| | | 675 | | | | | 680 | | | | | 685 | | | | | | | | |
| acc | ggt | tac | ttc | ctg | gaa | cct | caa | aat | ggg | atg | ttt | ggc | ggt | gga | tgt | 2112 | | | | |
| Thr | Val | Tyr | Phe | Leu | Glu | Pro | Gln | Asn | Gly | Met | Phe | Gly | Val | Gly | Cys | | | | | |
| | 690 | | | | | 695 | | | | | 700 | | | | | | | | | |
| gta | tat | gga | agg | aat | gat | gac | cgc | aga | ttt | ggg | ttc | ttc | tgt | cat | tct | 2160 | | | | |
| Val | Tyr | Gly | Arg | Asn | Asp | Asp | Arg | Arg | Phe | Gly | Phe | Phe | Cys | His | Ser | | | | | |
| 705 | | | | | 710 | | | | | 715 | | | | | 720 | | | | | |
| gct | cta | gag | ttt | atc | ctc | cag | aat | gaa | ttt | tct | cca | cat | ata | ata | cat | 2208 | | | | |
| Ala | Leu | Glu | Phe | Ile | Leu | Gln | Asn | Glu | Phe | Ser | Pro | His | Ile | Ile | His | | | | | |
| | | | | 725 | | | | | 730 | | | | | 735 | | | | | | |
| tgc | cat | gat | tgg | tca | agt | gct | ccg | gtc | gcc | tgg | cta | tat | aag | gaa | cac | 2256 | | | | |
| Cys | His | Asp | Trp | Ser | Ser | Ala | Pro | Val | Ala | Trp | Leu | Tyr | Lys | Glu | His | | | | | |
| | | | 740 | | | | | | 745 | | | | 750 | | | | | | | |
| tat | tcc | caa | tcc | aga | atg | gca | agc | act | cgg | gtt | gta | ttt | acc | atc | cac | 2304 | | | | |
| Tyr | Ser | Gln | Ser | Arg | Met | Ala | Ser | Thr | Arg | Val | Val | Phe | Thr | Ile | His | | | | | |
| | | 755 | | | | | 760 | | | | | 765 | | | | | | | | |
| aat | ctt | gaa | ttt | gga | gca | cat | tat | att | ggt | aaa | gca | atg | aca | tac | tgt | 2352 | | | | |
| Asn | Leu | Glu | Phe | Gly | Ala | His | Tyr | Ile | Gly | Lys | Ala | Met | Thr | Tyr | Cys | | | | | |
| | 770 | | | | | 775 | | | | | 780 | | | | | | | | | |
| gat | aaa | gcc | aca | act | gtt | tct | cct | aca | tat | tca | agg | gac | gtg | gca | ggc | 2400 | | | | |
| Asp | Lys | Ala | Thr | Thr | Val | Ser | Pro | Thr | Tyr | Ser | Arg | Asp | Val | Ala | Gly | | | | | |
| | | | | | 790 | | | | | 795 | | | | | 800 | | | | | |
| cat | ggc | gcc | att | gct | cct | cat | cgt | gag | aaa | ttc | tac | ggc | att | ctc | aat | 2448 | | | | |
| His | Gly | Ala | Ile | Ala | Pro | His | Arg | Glu | Lys | Phe | Tyr | Gly | Ile | Leu | Asn | | | | | |
| | | | | 805 | | | | | 810 | | | | | 815 | | | | | | |
| gga | att | gat | cca | gat | atc | tgg | gat | ccg | tac | act | gac | aat | ttt | atc | ccg | 2496 | | | | |
| Gly | Ile | Asp | Pro | Asp | Ile | Trp | Asp | Pro | Tyr | Thr | Asp | Asn | Phe | Ile | Pro | | | | | |
| | | | 820 | | | | | | | | | | 830 | | | | | | | |
| gtc | cct | tat | act | tgt | gag | aat | gtt | gtc | gaa | ggc | aag | agg | gct | gca | aaa | 2544 | | | | |
| Val | Pro | Tyr | Thr | Cys | Glu | Asn | Val | Val | Glu | Gly | Lys | Arg | Ala | Ala | Lys | | | | | |
| | | 835 | | | | | 840 | | | | | 845 | | | | | | | | |
| agg | gcc | ttg | cag | cag | aag | ttt | gga | tta | cag | caa | act | gat | gtc | cct | att | 2592 | | | | |
| Arg | Ala | Leu | Gln | Gln | Lys | Phe | Gly | Leu | Gln | Gln | Thr | Asp | Val | Pro | Ile | | | | | |
| | 850 | | | | | 855 | | | | | 860 | | | | | | | | | |
| gtc | gga | atc | atc | acc | cgt | ctg | aca | gca | cag | aag | gga | atc | cac | ctc | atc | 2640 | | | | |

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| | | | | | | | | | | | | | | | | |
|------------|-------------------|------------|-------------|------------|------------|------------|-----|------|------|------|-----|------|------|------|-----|------|
| acc | tac | gat | gag | cct | ctt | tct | cac | ctg | ata | tac | gct | ggc | tcc | gac | ttc | 2832 |
| Thr | Tyr | Asp | Glu | Pro | Leu | Ser | His | Leu | Ile | Tyr | Ala | Gly | Ser | Asp | Phe | |
| 930 | | | | | | 935 | | | | | 940 | | | | | |
| att | att | gtc | cct | tca | atc | ttt | gaa | ccc | tgt | ggc | tta | aca | caa | ctt | gtt | 2880 |
| Ile | Ile | Val | Pro | Ser | Ile | Phe | Glu | Pro | Cys | Gly | Leu | Thr | Gln | Leu | Val | |
| 945 | | | | | 950 | | | | | 955 | | | | | 960 | |
| gcc | atg | cgt | tat | gga | tcg | atc | cct | ata | gtt | cgg | aaa | acc | gga | gga | ctt | 2928 |
| Ala | Met | Arg | Tyr | Gly | Ser | Ile | Pro | Ile | Val | Arg | Lys | Thr | Gly | Gly | Leu | |
| | | | | 965 | | | | | 970 | | | | | 975 | | |
| tac | gac | act | gtc | ttc | gac | gta | gac | aat | gat | aag | gac | cgg | gct | cgg | tct | 2976 |
| Tyr | Asp | Thr | Val | Phe | Asp | Val | Asp | Asn | Asp | Lys | Asp | Arg | Ala | Arg | Ser | |
| | | | 980 | | | | | 985 | | | | | 990 | | | |
| ctt | ggt | ctt | gaa | cca | aat | ggg | ttc | agt | ttc | gac | gga | gcc | gac | agc | aat | 3024 |
| Leu | Gly | Leu | Glu | Pro | Asn | Gly | Phe | Ser | Phe | Asp | Gly | Ala | Asp | Ser | Asn | |
| | | 995 | | | | 1000 | | | | | | 1005 | | | | |
| ggc | gtg | gat | tat | gcc | ctc | aac | aga | gca | atc | ggc | gct | tgg | ttc | gat | gcc | 3072 |
| Gly | Val | Asp | Tyr | Ala | Leu | Asn | Arg | Ala | Ile | Gly | Ala | Trp | Phe | Asp | Ala | |
| 1010 | | | | | 1015 | | | | | 1020 | | | | | | |
| cgt | gat | tgg | ttc | cac | tcc | ctg | tgt | aag | agg | gtc | atg | gag | caa | gac | tgg | 3120 |
| Arg | Asp | Trp | Phe | His | Ser | Leu | Cys | Lys | Arg | Val | Met | Glu | Gln | Asp | Trp | |
| 1025 | | | | 1030 | | | | | 1035 | | | | | 1040 | | |
| tcg | tgg | aac | cgg | cct | gca | ctg | gac | tac | att | gaa | ttg | tac | cat | gcc | gct | 3168 |
| Ser | Trp | Asn | Arg | Pro | Ala | Leu | Asp | Tyr | Ile | Glu | Leu | Tyr | His | Ala | Ala | |
| | | | 1045 | | | | | 1050 | | | | | 1055 | | | |
| cga | aaa | ttc | tgacacccaa | ctgaaccaat | ggcaagaaca | agcgcatgtg | | | | | | | | | | 3217 |
| Arg | Lys | Phe | | | | | | | | | | | | | | |
| gggatcgact | acagtcatac | agggctgtgc | agatcgctctt | gcttcagtta | gtgccctctt | | | | | | | | | | | 3277 |
| cagttagttc | caagcgcaact | acagtcgtac | atagctgagg | atcctcttgc | ctcctccacc | | | | | | | | | | | 3337 |
| aggggaaaca | aagcagaaat | gcataagtgc | attgggaaga | cttttatgta | tattgttaaa | | | | | | | | | | | 3397 |
| tttttccttt | tcttttctt | ccctgcacct | ggaaatgggt | aagcgcatcg | ccgagataag | | | | | | | | | | | 3457 |
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| gcatgttagg | ctctctgac | atgtggaagc | tttgtttatar | gttacttatg | gttatatgg | | | | | | | | | | | 3577 |
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| <213> | Triticum aestivum | | | | | | | | | | | | | | | |
| <400> | 10 | | | | | | | | | | | | | | | |
| Asp | Ala | Leu | Tyr | Val | Asn | Gly | Leu | Glu | | | | | | | | |

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Lys Thr Trp Lys Lys Val Asp Glu Glu His Leu Tyr Met Thr Glu His
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 Gln Lys Arg Ala Ala Glu Gly Gln Met Val Val Asn Glu Asp Glu Leu
 65 70 75 80
 Ser Ile Thr Glu Ile Gly Met Gly Arg Gly Asp Lys Ile Gln His Val
 85 90 95
 Leu Ser Glu Glu Glu Leu Ser Trp Ser Glu Asp Glu Val Gln Leu Ile
 100 105 110
 Glu Asp Asp Gly Gln Tyr Glu Val Asp Glu Thr Ser Val Ser Val Asn
 115 120 125
 Val Glu Gln Asp Ile Gln Gly Ser Pro Gln Asp Val Val Asp Pro Gln
 130 135 140
 Ala Leu Lys Val Met Leu Gln Glu Leu Ala Glu Lys Asn Tyr Ser Met
 145 150 155 160
 Arg Asn Lys Leu Phe Val Phe Pro Glu Val Val Lys Ala Asp Ser Val
 165 170 175
 Ile Asp Leu Tyr Leu Asn Arg Asp Leu Thr Ala Leu Ala Asn Glu Pro
 180 185 190
 Asp Val Val Ile Lys Gly Ala Phe Asn Gly Trp Lys Trp Arg Leu Phe
 195 200 205
 Thr Glu Arg Leu His Lys Ser Asp Leu Gly Gly Val Trp Trp Ser Cys
 210 215 220
 Lys Leu Tyr Ile Pro Lys Glu Ala Tyr Arg Leu Asp Phe Val Phe Phe
 225 230 235 240
 Asn Gly Arg Thr Val Tyr Glu Asn Asn Gly Asn Asn Asp Phe Cys Ile
 245 250 255
 Gly Ile Glu Gly Thr Met Asn Glu Asp Leu Phe Glu Asp Phe Leu Val
 260 265 270
 Lys Glu Lys Gln Arg Glu Leu Glu Lys Leu Ala Met Glu Glu Ala Glu
 275 280 285
 Arg Arg Thr Gln Thr Glu Glu Gln Arg Arg Arg Lys Glu Ala Arg Ala
 290 295 300
 Ala Asp Glu Ala Val Arg Ala Gln Ala Lys Ala Glu Ile Glu Ile Lys
 305 310 315 320
 Lys Lys Lys Leu Gln Ser Met Leu Ser Leu Ala Arg Thr Cys Val Asp
 325 330 335
 Asn Leu Trp Tyr Ile Glu Ala Ser Thr Asp Thr Arg Gly Asp Thr Ile
 340 345 350
 Arg Leu Tyr Tyr Asn Arg Asn Ser Arg Pro Leu Ala His Ser Thr Glu
 355 360 365
 Ile Trp Met His Gly Gly Tyr Asn Asn Trp Ser Asp Gly Leu Ser Ile
 370 375 380
 Val Glu Ser Phe Val Lys Cys Asn Asp Lys Asp Gly Asp Trp Trp Tyr

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| | | | |
|---|-----------------|-----------------------------|-----|
| 385 | 390 | 395 | 400 |
| Ala Asp Val Ile Pro | Pro Glu Lys Ala | Leu Val Leu Asp Trp Val Phe | |
| | 405 | 410 | 415 |
| Ala Asp Gly Pro Ala Gly Asn Ala Arg Asn Tyr Asp Asn Asn Ala Arg | | | |
| | 420 | 425 | 430 |
| Gln Asp Phe His Ala Ile Leu Pro Asn Asn Asn Val Thr Glu Glu Gly | | | |
| | 435 | 440 | 445 |
| Phe Trp Ala Gln Glu Glu Gln Asn Ile Tyr Thr Arg Leu Leu Gln Glu | | | |
| | 450 | 455 | 460 |
| Arg Arg Glu Lys Glu Glu Thr Met Lys Arg Lys Ala Glu Arg Ser Ala | | | |
| | 465 | 470 | 475 |
| Asn Ile Lys Ala Glu Met Lys Ala Lys Thr Met Arg Arg Phe Leu Leu | | | |
| | 485 | 490 | 495 |
| Ser Gln Lys His Ile Val Tyr Thr Arg Thr Xaa Leu Lys Tyr Val Pro | | | |
| | 500 | 505 | 510 |
| Gly Thr Thr Val Asp Val Leu Tyr Asn Pro Ser Asn Thr Val Leu Asn | | | |
| | 515 | 520 | 525 |
| Gly Lys Ser Glu Gly Trp Phe Arg Cys Ser Phe Asn Leu Trp Met His | | | |
| | 530 | 535 | 540 |
| Ser Ser Gly Ala Leu Pro Pro Gln Lys Met Val Lys Ser Gly Asp Gly | | | |
| | 545 | 550 | 555 |
| Pro Leu Leu Lys Ala Thr Val Asp Val Pro Pro Asp Ala Tyr Met Met | | | |
| | 565 | 570 | 575 |
| Asp Phe Val Phe Ser Glu Trp Glu Glu Asp Gly Ile Tyr Asp Asn Arg | | | |
| | 580 | 585 | 590 |
| Asn Gly Met Asp Tyr His Ile Pro Val Ser Asp Ser Ile Glu Thr Glu | | | |
| | 595 | 600 | 605 |
| Asn Tyr Met Arg Ile Ile His Ile Ala Val Glu Met Ala Pro Val Ala | | | |
| | 610 | 615 | 620 |
| Lys Val Gly Gly Leu Gly Asp Val Val Thr Ser Leu Ser Arg Ala Ile | | | |
| | 625 | 630 | 635 |
| Gln Asp Leu Gly His Thr Val Glu Val Ile Leu Pro Lys Tyr Asp Cys | | | |
| | 645 | 650 | 655 |
| Leu Asn Gln Ser Ser Val Lys Asp Leu His Leu Tyr Gln Ser Phe Ser | | | |
| | 660 | 665 | 670 |
| Trp Gly Gly Thr Glu Ile Lys Val Trp Val Gly Arg Val Glu Asp Leu | | | |
| | 675 | 680 | 685 |
| Thr Val Tyr Phe Leu Glu Pro Gln Asn Gly Met Phe Gly Val Gly Cys | | | |
| | 690 | 695 | 700 |
| Val Tyr Gly Arg Asn Asp Asp Arg Arg Phe Gly Phe Phe Cys His Ser | | | |
| | 705 | 710 | 715 |
| Ala Leu Glu Phe Ile Leu Gln Asn Glu Phe Ser Pro His Ile Ile His | | | |
| | 725 | 730 | 735 |

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Cys His Asp Trp Ser Ser Ala Pro Val Ala Trp Leu Tyr Lys Glu His
 740 745 750
 Tyr Ser Gln Ser Arg Met Ala Ser Thr Arg Val Val Phe Thr Ile His
 755 760 765
 Asn Leu Glu Phe Gly Ala His Tyr Ile Gly Lys Ala Met Thr Tyr Cys
 770 775 780
 Asp Lys Ala Thr Thr Val Ser Pro Thr Tyr Ser Arg Asp Val Ala Gly
 785 790 795 800
 His Gly Ala Ile Ala Pro His Arg Glu Lys Phe Tyr Gly Ile Leu Asn
 805 810 815
 Gly Ile Asp Pro Asp Ile Trp Asp Pro Tyr Thr Asp Asn Phe Ile Pro
 820 825 830
 Val Pro Tyr Thr Cys Glu Asn Val Val Glu Gly Lys Arg Ala Ala Lys
 835 840 845
 Arg Ala Leu Gln Gln Lys Phe Gly Leu Gln Gln Thr Asp Val Pro Ile
 850 855 860
 Val Gly Ile Ile Thr Arg Leu Thr Ala Gln Lys Gly Ile His Leu Ile
 865 870 875 880
 Lys His Ala Ile His Arg Thr Leu Glu Ser Asn Gly Gln Val Val Leu
 885 890 895
 Leu Gly Ser Ala Pro Asp His Arg Ile Gln Gly Asp Phe Cys Arg Leu
 900 905 910
 Ala Asp Ala Leu His Gly Val Tyr His Gly Arg Val Lys Leu Val Leu
 915 920 925
 Thr Tyr Asp Glu Pro Leu Ser His Leu Ile Tyr Ala Gly Ser Asp Phe
 930 935 940
 Ile Ile Val Pro Ser Ile Phe Glu Pro Cys Gly Leu Thr Gln Leu Val
 945 950 955 960
 Ala Met Arg Tyr Gly Ser Ile Pro Ile Val Arg Lys Thr Gly Gly Leu
 965 970 975
 Tyr Asp Thr Val Phe Asp Val Asp Asn Asp Lys Asp Arg Ala Arg Ser
 980 985 990
 Leu Gly Leu Glu Pro Asn Gly Phe Ser Phe Asp Gly Ala Asp Ser Asn
 995 1000 1005
 Gly Val Asp Tyr Ala Leu Asn Arg Ala Ile Gly Ala Trp Phe Asp Ala
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 Arg Asp Trp Phe His Ser Leu Cys Lys Arg Val Met Glu Gln Asp Trp
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 Arg Lys Phe

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<211> 728

WO 00/66745

PCT/AU00/00385

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<212> DNA

<213> Triticum sp.

<400> 11

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 gagatctcca cgccagagcg ttgtattcca atttttagttc tttccccgtg aggaggggag 180
 gctaggcggg cgaggcagag gggatagggc agtcgccgct gcgtggtgga ctgactggtg 240
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 cggccgcggc ggccgctcgc cgcaggtacg ggtgattatg gttcttgatt cggtcggttc 420
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 aaaaaaaaag gtttatagtg attttgattt ctttcatctc gggaacattt ttatatctgg 540
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 tgagctgga ttcatactgc ttaaaacgac gtgattttta ttgctggaag aggtaaagaa 660
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<211> 2446

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ttgatatata ttgtgaagtc acttaagcct tggtaaaacg tagaaactta gttccgcaac 480
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attactgagt acaatacaga gcaccgaaaa gctgtatcct tcctacttcc ttatgtttat 660
ctgtgttcct tgtctagtta atgttccacc ggatgcctat atgatggact ttgttttctc 720
cgagtgggaa gaagatggga tctatgacaa caggaatggg atggactatc atattcctgt 780

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ttctgattca attgaaacag agaattacat gcgtattatc cacattgccg ttgagatggc 840
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atcttgatt cagcgcgta ctttcagttt ctttactact agcttatttg gtgcattggg 180
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tctcgaggtc ttacattgc tgggtgctctt taccocgact ttctggcgtg aatgatggag 780
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<210> 16
<211> 1592
<212> DNA
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| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
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| atcccttgtg | aacgaataaa | catcaaacgt | tttgtttata | aaaagttgct | tactatttgt | 720 |
| ttttgtttac | ttcaaaacaa | aagtctgaaa | atgaagtgtt | tggttcctag | gtggttttgc | 780 |
| ttggttcagc | tccagatcat | cgaatacaa | gcgatttttg | cagattggcc | gatgctcttc | 840 |
| acggtgttta | ccacggtagg | gtgaagcttg | ttctaacct | cgatgagcct | ctttctcacc | 900 |
| tggtgagctc | caatatecta | cacaccatct | agccagccct | tcattatggg | agctggagac | 960 |
| tactttataa | tttaggttga | tgatcgatca | tgctgcagat | atacgctggc | tccgacttca | 1020 |
| ttattgtccc | ttcaatcttc | gaaccctgtg | gcttaacaca | acttgttgcc | atgcgttatg | 1080 |
| gatcgatccc | tatagttcgg | aaaaccggag | gtgtgtgact | atttctctcc | attatgctgc | 1140 |
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| gactttacga | cactgtcttc | gacgtagaca | atgataagga | ccgggctcgg | tctcttggtc | 1260 |
| ttgaaccaa | tgggttcagt | ttcgacggag | ccgacagcaa | cggcgtggat | tatgccctca | 1320 |
| acaggcaagt | atcgttcctc | aattagccct | gaattcagca | gtagtgctag | gttatttacc | 1380 |
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| actacattga | attgtaccat | gccgctcgaa | aattctgaca | cccaactgaa | ccaatggcaa | 1560 |
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